

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 03:05:20 ; Search time 2327 Seconds
(without alignments)
8245.924 Million cell updates/sec

Title: US-10-010-942B-1
Perfect score: 396
Sequence: 1 atgatgagtcctgccagtt.....gcaccaagctggaatcaaa 396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_to.*
- 11: gb_ats.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	396	100.0	396	6	AX458138 Sequence
2	388	98.0	428	10	MUSIGKCLM
3	384.8	97.2	930	10	AY571288 Mus muscu
4	380.2	96.0	393	10	AF045492 Mus muscu
5	380.2	96.0	393	10	AF045493 Mus muscu
6	374.4	94.5	1034	10	BC028925 Mus muscu
7	370.8	93.6	393	10	MUSICKCJ
8	370.6	93.6	717	6	CQ829526 Sequence
9	365.6	92.3	927	10	MUSILC
10	362.4	91.5	423	10	MUSIGMVA
11	361	91.2	393	6	AR452630
12	361	91.2	393	6	AR452631
13	359.4	90.8	396	10	AF157686
14	359.2	90.7	408	10	MMIGKEAD
15	340	85.9	1008	10	BC031498
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18	335.4	84.7	426	6	AR532506
19	335.4	84.7	426	6	AR532511

20	335.4	84.7	426	6	AX208063
21	335.4	84.7	426	6	AX208069
22	333.6	84.2	405	10	MMRIGLC
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24	332	83.8	356	10	MUSIGKVRA
25	328.8	83.0	959	10	RATIGK132A
26	323.8	81.8	336	10	AF143910
27	322.2	81.4	1135	6	BD244502
28	322.2	81.4	1135	6	AR454911
29	319.6	80.7	660	6	AR07556
30	319	80.6	336	10	MUSABLIGHT
31	319	80.6	336	10	MUSIGLDB
32	319	80.6	336	10	AF486644
33	319	80.6	339	10	MMU223533
34	319	80.6	339	10	S50912
35	319	80.6	339	10	AF083187
36	317.4	80.2	328	10	MMU28859
37	317.4	80.2	846	10	MUSALC
38	317.4	80.2	855	10	MUSALCA
39	315.8	79.7	336	10	MMALCVR19
40	315.8	79.7	339	10	MUSIGKCOJ
41	315.8	79.7	357	10	MUSIGKSG2
42	315.8	79.7	366	10	AY556405
43	315.8	79.7	738	12	AF064776
44	313.2	79.1	660	6	A07560
45	312.8	79.0	336	6	AR131300

ALIGNMENTS

RESULT 1
AX458138
LOCUS AX458138 396 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 1 from Patent WO0246237.
ACCESSION AX458138
VERSION AX458138.1 GI:21724896
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Basi, G., Saldanha, J. and Yednock, T.
TITLE Humanized antibodies that recognize beta amyloid peptide
JOURNAL Patent: WO 0246237-A 1 13-JUN-2002;
Neuralab Limited (BM); Wyeth (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:10090"
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/note="unnamed protein product"
/codon_start=1
/protein_id="CAD38344.1"
/db_xref="GI:21724897"
/translation="MMSPAQFLFLVLWIRETNQVVMVTQPLTSLVTIGOPASISCK
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Best Local Similarity 100.0%; Pred. No. 4.7e-120; Indels 0; Gaps 0;
Matches 396; Conservative 0; Mismatches 0;
Qy 1 ATGATGAGTCTGCCAGTCTCTCTTTCTGTAGTCTCTGGATTTCGGAAACCAACCGT 60
Db 1 ATGATGAGTCTGCCAGTCTCTCTTTCTGTAGTCTCTGGATTTCGGAAACCAACCGT 60
Qy 61 TATGTTGTGATGACCCAGACTCCACTCTTGTGCGGTACCATGTTGGACACACCGCTCC 120

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Db      121  ATCTCTTGAAGTCAAGTCAGAGCTCTTAGATAGTAGTGAGTGAAGACATATTTGAATTGG 180
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Db      181  TTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGTTGTTCTAAACTGGAC 240
QY      241  TCTGGAGTCCCTGACAGCTTCACTGGCAGTGCAGGACAGATTTTACACTGAAATC 300
Db      241  TCTGGAGTCCCTGACAGCTTCACTGGCAGTGCAGGACAGATTTTACACTGAAATC 300
QY      301  ACAGAGTAGAGCTTGAGGATTTGGACATTTATTTATGCTGCAAGGTACACATTTTCT 360
Db      301  ACAGAGTAGAGCTTGAGGATTTGGACATTTATTTATGCTGCAAGGTACACATTTTCT 360
QY      361  CGGAGCTTCGGTGGAGGCCACCAAGCTGGAAATCAAA 396
Db      361  CGGAGCTTCGGTGGAGGCCACCAAGCTGGAAATCAAA 396

RESULT 2
MUSIGKCLM
LOCUS      Mouse IgMk rearranged kappa light-chain mRNA variable region
DEFINITION (V-J-kappa) anti-DNA autoantibody.
ACCESSION M20830
VERSION    1
KEYWORDS   V-region; autoantibody; immunoglobulin kappa-chain; immunoglobulin
SOURCE     Mus musculus
ORGANISM   Mus musculus (house mouse)
REFERENCE  1 (bases 1 to 428)
AUTHORS    Kofler R., Strohal R., Balderas R.S., Johnson M.E., Noonan D.J.,
           Duchosal M.A., Dixon F.J. and Theofilopoulos A.N.
TITLE      Immunoglobulin kappa light chain variable region gene complex
           organization and immunoglobulin genes encoding anti-DNA
           autoantibodies in lupus mice
JOURNAL    J. Clin. Invest. 82 (3), 852-860 (1988)
MEDLINE    8831394
PUBMED     3138286
COMMENT    Original source text: Mouse (strain (NZBxW) F-1) spleen hybridoma
           cell line BXW-DNA14, cDNA to mRNA.
           Draft entry and computer-readable sequence [1] kindly submitted by
           R.Kofler 28-JUL-1988.
FEATURES   Location/Qualifiers
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                       /db_xref="GI:196940"
                       /translation="MMSPAQFLFLVLWIRETNGDVVMTQPTLTLSVTIGQPASISCK
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                       /note="Ig light chain signal peptide"
            mat_peptide 93..>428
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                       Query Match      98.0%; Score 388; DB 10; Length 428;
                       Best Local Similarity 98.7%; Pred. No. 2.2e-117;
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QY      1  ATGATGAGTCCTGCCAGTTCCTGTTCTGTTAGTGCTCTGGATTTCGGAAACCAACCGT 60
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Db      93  GATGTTGTGATGACCCAGACTCCACTCACTTTGTGCGGTACCATTTGGAGCAACACGCTCC 152
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Db      153  ATCTCTTCAAGTCAAGTCAGAGCTCTTAGATAGTAGTGAGTGAAGACATATTTGAATTGG 212
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Db      213  TTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGTTGTTCTAAACTGGAC 272
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Db      273  TCTGGAGTCCCTGACAGCTTCACTGGCAGTGCAGGACAGATTTTACACTGAAATC 332
QY      301  AGCAGATAGAGCTTGAGGATTTGGGACATTTATTTATGCTGCAAGGTACACATTTTCT 360
Db      333  AGCAGATAGAGCTTGAGGATTTGGGAGTTTATTTATGCTGCAAGGTACACATTTTCT 392
QY      361  CGGAGCTTCGGTGGAGGCCACCAAGCTGGAAATCAAA 396
Db      393  CGGAGCTTCGGTGGAGGCCACCAAGCTGGAAATCAAA 428

RESULT 3
AY571288
LOCUS      Mus musculus anti-CMV coat protein monoclonal antibody CymwV-L 23
DEFINITION immunoglobulin light chain variable region mRNA, complete cds.
ACCESSION AY571288
VERSION    1
KEYWORDS   AY571288.1 GI:50346341
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 930)
AUTHORS    Wang, H.L., Lee, C.H. and Hsu, H.T.
TITLE      Molecular Cloning and Sequencing of Heavy and Light Chain cDNAs
           from Papaya Ringspot and Cymbidium mosaic viruses-Specific
           Monoclonal Antibodies
JOURNAL    Zhi Wu Bing Li Xue Hui Kan 13 (2004) In press
REFERENCE  2 (bases 1 to 930)
AUTHORS    Wang, H.L., Lee, C.H. and Hsu, H.T.
TITLE      Direct Submission
JOURNAL    Submitted (11-MAR-2004) Graduate Institute of Biology Science,
           National Kaohsiung Normal University, 116, Ho Ping 1Rd, Kaohsiung
           802, Taiwan
FEATURES   Location/Qualifiers
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Best Local Similarity 98.0%; Pred. No. 8.5e-115;
Matches 385; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 4 ATGAGTCCTGCCAGTCTCTGTTCTCTGTTAGTCTCTGGAATCGGAAACCAACGGTTAT 63
DB 1 ATGAGTCCTGCCAGTCTCTGTTCTCTGTTAGTCTCTGGAATCGGAAACCAACGGTGAT 60
QY 64 GTTGTATGATGCCAGTCTCCTACTCTGTTGTGGTTACCATTTGGACCAACGAGCTCCATC 123
DB 61 GTTGTATGATGCCAGTCTCCTACTCTGTTGTGGTTACCATTTGGACCAACGAGCTCCATC 120
QY 124 TCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGATGGAAGACATATTTGAATTTGGTTG 183
DB 121 TCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGATGGAAGACATATTTGAATTTGGTTG 180
QY 184 TTACAGAGCCAGCCAGTCTCAAGCCGCTAATCTATCTGTTGTCTAACTGGACTCT 243
DB 181 TTACAGAGCCAGCCAGTCTCAAGCCGCTAATCTATCTGTTGTCTAACTGGACTCT 240
QY 244 GGAGTCCCTGACAGGTTCACTGACAGTGGATCAGGACAGATTTTACATGAAATCAGC 303
DB 241 GGAGTCCCTGACAGGTTCACTGACAGTGGATCAGGACAGATTTTACATGAAATCAGC 300
QY 304 AGAATAGAGGCTGAGGATTTGGGAGTTTATTATTGCTGCAAGGTACACATTTTCTCGG 363
DB 301 AGAATAGAGGCTGAGGATTTGGGAGTTTATTATTGCTGCAAGGTACACATTTTCTCGG 360
QY 364 ACCTTCGGTGGAGCCACCAAGCTGGAATCAAA 396
DB 361 ACCTTCGGTGGAGCCACCAAGCTGGAATCAAA 393
RESULT 6
BC028925 1034 bp mRNA linear ROD 12-OCT-2004
LOCUS Mus musculus cDNA clone MGC:25820 IMAGE:4164906, complete cds.
DEFINITION BC028925
ACCESSION BC028925
VERSION BC028925.1 GI:20809356
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1034)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klauser,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K.,
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Hopkins,R.P., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettner,M., Maman,A., Rodrigues,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,
Schnerker,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1034)
Director MGC Project.
Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapps@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegad, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 30 Row: m Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
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/notes="Vector: pCMV-SPORT6"
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SQSLDSDGKTYLWLLQRPQSPKRLIYLVSKLDSGVPDRFTSGSGTDFTLKISR
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Query Match 94.5%; Score 374.4; DB 10; Length 1034;
Best Local Similarity 98.2%; Pred. No. 7.8e-113;
Matches 389; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 ATGATGAGTCCTGCCAGTCTCTGTTCTCTGTTAGTCTCTGGAATCGGAAACCAACGGGT 60
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Db      43  ATGATGAGTCTGCCAGTTCCTGTTCTGCTAGTCTCTGGATTCGGGAAACCAACGGT 102
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Qy      181  TTGTTACAGAGCCAGCCAGTCTCCAAAGCCCTAATCTATCTGCTGCTAACTGGAC 240
Db      223  TTGTTACAGAGCCAGCCAGTCTCCAAAGCCCTAATCTATCTGCTGCTAACTGGAC 282
Qy      241  TCTGGAGTCCCTGACAGGTTTCACTGTCAGTGGATCAGGACAGATTTTACACTGAAATC 300
Db      283  TCTGGAGTCCCTGACAGGTTTCACTGTCAGTGGATCAGGACAGATTTTACACTGAAATC 342
Qy      301  ACCAGATAGAGCTGAGGATTTGGACATTTATTTATTTGCTGGCAGAGTACATTTTCT 360
Db      343  ACCAGATAGAGCTGAGGATTTGGACATTTATTTATTTGCTGGCAGAGTACATTTTCT 402
Qy      361  CGAGCTTCGGTGGAGCCACCAAGCTGGAATCAAA 396
Db      403  -GCAGTTCCGGTGGAGCCACCAAGCTGGAATCAAA 437

RESULT 7
MUSICKCJ
LOCUS      MUSICKCJ      393 bp      mRNA      linear      ROD 27-APR-1993
DEFINITION Mouse ig active kappa-chain VOX1-J2 region anti-dextran mRNA,
hybridoma 42.48.12.2.
ACCESSION M17722.1 GI:194086
VERSION   1
KEYWORDS  C-region; J-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; processed gene.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 393)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Akolkar,P.N., Sikder,S.K., Bhattacharya,S.B., Liao,J., Gruezo,F.,
Morrison,S.L. and Kabat,E.A.
TITLE     Different VL and VH germ-line genes are used to produce similar
combining sites with specificity for alpha(1----6)dextran
JOURNAL   J. Immunol. 138 (12), 4472-4479 (1987)
MEDLINE   87224123
PUBMED    2438345
COMMENT   Original source text: Mouse (C57BL) hybridoma cell line 42.48.12.2,
CDNA to mRNA.
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55..>393
ORIGIN     /product="Ig kappa light chain VOX1-J2-region"
Chromosome 6.
Query Match 93.6%; Score 370.8; DB 10; Length 393;
Best Local Similarity 96.9%; Pred. No. 1.1e-111;
Matches 378; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy      7  AGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGGATTCGGGAAACCAACGGTTATGTT 66
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Qy      127  TGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 186
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Qy      187  CAGAGCCAGGCGAGTCTCCAAAGCCCTAATCTATCTGCTGCTAACTGGAC 246
Db      181  CAGAGCCAGGCGAGTCTCCAAAGCCCTAATCTATCTGCTGCTAACTGGAC 240
Qy      247  GTCCCTGACAGGTTCACTGTCAGTGGATCAGGACAGATTTTACACTGAAATCAGCAGA 306
Db      241  GTCCCTGACAGGTTCACTGTCAGTGGATCAGGACAGATTTTACACTGAAATCAGCAGA 300
Qy      307  ATAGAGGCTGAGGATTTGGGACTTTATTTATTTGCTGGCAAGGTACACATTTTCTCGGACG 366
Db      301  GTGAGGCTGAGGATTTGGGACTTTATTTATTTGCTGGCAAGGTACACATTTTCTCGGACG 360
Qy      367  TTCGGTGGAGGCCAACAGCTGGAATCAAA 396
Db      361  TTCGGAGGGGGGACCAAGCTGGAATAAAA 390

RESULT 8
CQ829526
LOCUS      CQ829526      717 bp      DNA      linear      PAT 05-JUL-2004
DEFINITION Sequence 44 from Patent WO2004052932.
ACCESSION CQ829526
VERSION   CQ829526.1 GI:49732837
KEYWORDS  Mus musculus (house mouse)
SOURCE    Mus musculus
ORGANISM  Mus musculus
REFERENCE 1
AUTHORS   Barske,C., Mir,A.K., Oertle,T., Schnell,L., Schwab,M.E.,
Vitaliti,A. and Zurini,M.
TITLE     Nogo a binding molecules and pharmaceutical use thereof
JOURNAL   Patent: WO 2004052932-A 44 24-JUN-2004;
Novartis AG (CH)
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Matches 379; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy      4  ATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGGATTCGGGAAACCAACGGTTAT 63
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Qy      64  GTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTTGGACCAACAGCCTCCATC 123
Db      61  GTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTTGGACCAACAGCCTCCATC 120
Qy      124  TCTTGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 183
Db      121  TCTTGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 180
Qy      184  TTACAGAGGCCAGGCCAGTCTCCAAAGCCCTAATCTATCTGCTGCTAACTGGACTCT 243

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181 TTACAGAGCCGAGCCGAGTCTCCAAAGCGCCTAAATCTATCTGGTGTCTAAACTGGACTCT 240
244 GGAGTCCCTGACAGGTTTCACTGSCAGTGGATCAGGGACAGATTTTACACTGGAATCAGC 303
241 GGAGTCCCTGACAGGTTTCACTGSCAGTGGATCAGGGACGATTTTACACTGGAATCAGC 300
304 AGAATAGAGGCTGAGGATTTGGGACTTTTATTATTGCTGGCAAGGTACACATTTTCTCGG 363
301 AGAGTGGAGGCTGAGGATTTGGGACTTTTATTATTGCTGGCAAGGTACACATTTTCTCAG 360
364 AGCTTCGGTGGAGGACCAAGCTGGAAATCAAA 396
361 ACCTTCGGTGGAGGCCCAAGCTGGAAATCAAA 393

RESULT 9
MUSILC
LOCUS
DEFINITION
Mus sp. mRNA for immunoglobulin light chain, complete cds,
monoclonal antibody to potato virus Y coat protein.
ACCESSION
D17386
VERSION
D17386.1 GI:688418
KEYWORDS
SOURCE
Mus sp.
ORGANISM
Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 927)
AUTHORS
Onshima,K., Matsuura,A., Nakaya,T., Shikata,E., Kikuchi,K. and
Kimura,I.
TITLE
Molecular cloning and nucleotide sequences of heavy and light chain
genes of a monoclonal antibody to potato virus Y coat protein
Ann. Phytopathol. Soc. Jpn. 60, 600-607 (1994)
2 (bases 1 to 927)
JOURNAL
Onshima,K.
REFERENCE
Direct Submission
AUTHORS
Submitted (09-AUG-1993) Kazusato Ohshima, Faculty of Agriculture,
Saga University, Laboratory of Plant Virology; 1 Honjo-machi, Saga,
Sage 840, Japan (Tel:81-952-24-5191(ex.2730), Fax:81-952-22-6274)
JOURNAL
Sage 840, Japan
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927
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Best Local Similarity 95.2%; Pred. No. 6.5e-110;
Matches 377; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
1 ATGATGAGTCCCTGCCAGTCCCTGTTTCTGTTAGTCTCTGGATTTCGGGAACCAACGCT 60
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361 CGGACGTTTCGGTGGAGGCCACCAAGCTGGAAATCAAA 396
361 TTCACGTTTCGGCTCGGGACAAAAGTTGGAATATAAA 396

MUSIGMVA
LOCUS
DEFINITION
Mouse immunoglobulin light chain variable region.
ACCESSION
L26541
VERSION
L26541.1 GI:473478
KEYWORDS
V-region; immunoglobulin; light chain.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 423)
AUTHORS
Weiner,G.J. and Kaminski,M.S.
TITLE
Anti-idiotypic antibodies recognizing stable epitopes limit the
emergence of idiotype variants in a murine B cell lymphoma
J. Immunol. 144 (6), 2436-2445 (1990)
JOURNAL
90187894
MEDLINE
1690244
PUBMED
REFERENCE
2 (bases 1 to 423)
AUTHORS
Weiner,G.J. and Hillstrom,J.R.
TITLE
Bispecific anti-idiotypic/anti-CD3 antibody therapy of murine B cell
lymphoma
J. Immunol. 147 (11), 4035-4044 (1991)
JOURNAL
92043796
MEDLINE
1834746
PUBMED
REFERENCE
3 (bases 1 to 423)
AUTHORS
Weiner,G.J., Kostelny,S.A., Hillstrom,J.R., Cole,M.S., Link,B.K.,
Wang,S.B. and Tso,J.Y.
TITLE
The role of T cell activation in anti-CD3 x antitumor bispecific
antibody therapy
J. Immunol. 152 (5), 2385-2392 (1994)
JOURNAL
94179820
MEDLINE
8133049
PUBMED
COMMENT
Original source text: Mus musculus (individual isolate MS9A6)
female cDNA to mRNA.
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Qy	61	TATGTTGTGATGACCCAGACTCCACTCATTGTTGTCGGTTACCAATTGGACACACGCTCC	120							
Db	88	GATGTTGTGATGACCCAGACTCCCGTCTCACTTGTTCGGTTACCAATTGGACACACCGCTCC	147							
Qy	121	ATCTCTTTGCAAGTCAAGTTCAGAGCTCTTAGATAGTGTGATGAAAGACATATTTGCAATTGG	180							
Db	148	ATCTCTTTCAGTCAAGTTCAGAGCTCTTAGAGGGTGTATGAAAGACATATTTGCAATTGG	207							
Qy	181	TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAACTATCTATCTGGTGTCTTAAACTGGAC	240							
Db	208	TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAACTATCTATCTGGTGTCTTAAACTGGAC	267							
Qy	241	TCGGAGTCCCTGCACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATC	300							
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Db	328	AGCAGATGAGGCTGAGGATTTTCGGAAATTTATTATTGCTGCGAAGGTACACATTTTCCT	387							
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Db	388	CTCAGTTCCGGGCTGGGACAAAGCTGGAGCTGAAA	423							
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AR452630										
LOCUS	AR452630	393 bp	DNA	linear	PAT 20-FEB-2004					
DEFINITION	Sequence 16 from patent US 6677436.									
ACCESSION	AR452630									
VERSION	AR452630.1 GI:42684511									
KEYWORDS	.									
SOURCE	Unknown.									
ORGANISM	Unknown.									
REFERENCE	Unclassified.									
AUTHORS	1 (bases 1 to 393)									
TITLE	Sato,K., Adachi,H. and Yabuta,N.									
JOURNAL	Humanized antibody against human tissue factor (TF) and process of production of the humanized antibody									
FEATURES	Patent: US 6677436-A 16 13-JAN-2004;									
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Db	61	GTTGTGATGACCCAGACTCCCACTCACTTGTTCGGTTACCAATTGGACACACGCTCCGTC	120							
Qy	124	TCTTGCAAGTCAAGTTCAGAGCTCTTAGATAGTGTGAAAGACATATTTGCAATTGGTTG	183							
Db	121	TCTTGCAAGTCAAGTTCAGAGCTCTTAGATAGTGTGAAAGACATATTTGCAATTGGTTG	180							

LOCUS AF157686 396 bp mRNA linear ROD 30-MAY-2000
DEFINITION Mus musculus immunoglobulin kappa light chain variable region mRNA,
partial cds.
ACCESSION AF157686
VERSION AF157686.1 GI:5306067
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 396)
AUTHORS Park,O.Y., Jin,Y.H., Lee,M., Shin,H.J., Kim,H.I., Cho,H., Yun,C.W.,
Youn,J.K. and Park,S.
TITLE Characterization and gene cloning of monoclonal antibody specific
for the hepatitis B virus X protein
JOURNAL Hybridoma 19 (1), 73-80 (2000)
MEDLINE 2029330
PUBMED 10768843
REFERENCE 2 (bases 1 to 396)
AUTHORS Park,O.Y., Jin,Y.H., Lee,M., Kim,H.I., Youn,J.K. and Park,S.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1999) Microbiology, Ajou Univ. School of
Medicine, Paldalku, Suwon, Kyngkido 441-749, South Korea
FEATURES
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LOCUS AF157686 396 bp mRNA linear ROD 13-MAY-1993
DEFINITION Mus musculus encoding immunoglobulin kappa light chain.
ACCESSION Z17401
VERSION Z17401.1 GI:52148
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 408)
AUTHORS Medina,C.A. and Teale,J.M.
TITLE Restricted kappa chain expression in early ontogeny: biased
utilization of V kappa exons and preferential V kappa-J kappa
recombinations
JOURNAL J. Exp. Med. 177 (5), 1317-1330 (1993)
MEDLINE 93240113
PUBMED 8478611
REFERENCE 2 (bases 1 to 408)
AUTHORS Medina,C.A.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1992) Medina C. A., University of Texas Health
Science Center at San Antonio, Microbiology, 7703 Floyd Curl Dr.,
San Antonio, TX, USA, 78284
FEATURES
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Matches 373; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 ATGATGAGTCTGCCAGTCTCTGTTCTGTAGTCTCTGGATTGCGGAACCAACGCT 60
DB 13 ATGATGAGTCTGCCAGTCTCTGTTCTGTAGTCTCTGGATTGCGGAACCAACGCT 72
QY 61 TATGTTGTGATGACCCAGACTCCACTCACTTTGTGCGTTACCATTTGGACACAGCCTCC 120
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Db 373 TACAGTTCGGAGGGGGGACCAAGCTGGAAATAAA 408
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RESULT 15

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DEFINITION Mus musculus cDNA clone MGC:27817 IMAGE:3482714, complete cds.
ACCESSION BC031498
VERSION MGC.

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 1008)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL

12477932

2 (bases 1 to 1008)

REFERENCE

Strausberg, R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 35 Row: f Column: 15

This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

FEATURES

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CDS

misc_feature

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Best Local Similarity 91.2%; Pred. No. 2.1e-101;
Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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QY 61 TATGTTGTGATGACCCAGACTCCACTCATCTTTGTGGTTACCATTTGGACACACCTCC 120
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QY 241 TCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATGAGGACAGAGATTTTACACTGAAATC 300
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Db 256 TCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATGAGGACAGAGATTTTACACTGAAATC 315
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Db 316 AGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTACTGTTGAGAGTACACATTTTCCG 375
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QY 361 CGGAGCTTCGGTGGAGGACCAAGCTGGAAATCAAA 396
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Db 376 TACAGTTCGGAGGGGGGACCAAGCTGGAGATAAAA 411
|||||

Search completed: September 26, 2005, 05:47:58

Job time : 2331 secs

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OM protein - protein search, using sw model

Run on: September 26, 2005, 05:09:16 ; Search time 86 Seconds
(without alignments)
593.632 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLVIRETNG.....CWQGHFRPTFGGKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	692	100.0	132	5	Abg76923 Mouse 3D6
2	692	100.0	132	8	Adr88406 Murine 3D
3	655	94.7	238	8	Adm72033 Chimeric
4	653	94.4	238	8	Adp45549 Mouse bin
5	650	93.9	135	5	Abb79729 Anti-Strc
6	644	93.1	239	6	Abp58274 Humanised
7	641	92.6	132	2	Aar12361 Light (ka
8	641	92.6	133	8	Ado00819 Antibody
9	641	92.6	133	8	Ado43845 Light cha
10	640	92.5	132	5	Abg76925 Humanised
11	640	92.5	132	8	Adr88409 Humanised
12	639	92.3	131	2	Aar12239 Mouse Mab
13	636	91.9	132	6	Abg74244 Mouse ant
14	630	91.0	132	5	Abg76931 Humanised
15	630	91.0	132	8	Adr88415 Humanised
16	628	90.8	132	2	Aar24712 Sequence
17	606	87.6	142	4	Aae07032 Murine an
18	606	87.6	142	8	Adg89324 Mouse imm
19	595	86.0	239	2	Aar24811 Sequence
20	589	85.1	239	7	Adp47025 Rat Prote
21	573	82.8	113	8	Adq76076 Heterorec
22	571	82.5	113	4	Aae03751 Murine PS
23	571	82.5	113	8	Adq76088 Heterorec
24	571	82.5	218	4	Aae03756 Chimeric
25	570	82.4	113	8	Adq76078 Heterorec

26	569	82.2	113	8	ADQ76082	Adq76082 Heterorec
27	569	82.2	113	8	ADQ76086	Adq76086 Heterorec
28	568	82.1	112	8	ADQ76094	Adq76094 Heterorec
29	568	82.1	113	8	ADQ76092	Adq76092 Heterorec
30	568	82.1	113	8	ADQ76080	Adq76080 Heterorec
31	566	81.8	113	8	ADG25828	Adg25828 Anti-CD30
32	566	81.8	113	8	ADQ76090	Adq76090 Heterorec
33	566	81.8	114	8	ADG25839	Adg25839 Anti-CD30
34	563	81.4	112	8	ADQ76074	Adq76074 Heterorec
35	562	81.2	113	8	ADQ76084	Adq76084 Heterorec
36	562	80.9	353	2	AAy06273	Aay06273 Anti Fc a
37	560	80.9	112	4	AAE06946	Aae06946 Murine 1D
38	560	80.9	112	4	AAU09918	Aau09918 Murine MA
39	560	80.9	112	5	ABG75527	Abg75527 Mouse mAb
40	560	80.9	112	5	ADF98231	Adf98231 Murine MA
41	560	80.9	112	7	ABR61865	AbR61865 Mouse MAb
42	560	80.9	112	8	ADQ31246	Adq31246 Murine 1A
43	560	80.9	112	8	ADQ89231	Adq89231 Mouse imm
44	560	80.9	122	8	ADJ95990	Adj95990 Immunoglo
45	560	80.9	130	8	ADJ95992	Adj95992 Immunoglo

ALIGNMENTS

RESULT 1
ABG76923

ID ABG76923 standard; protein; 132 AA.

XX AC ABG76923;

XX DT 05-NOV-2002 (first entry)

XX DE Mouse 3D6 VL protein.

XX KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW neotropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta.

XX OS Mus musculus.

XX PN WO200246237-A2.

XX PD 13-JUN-2002.

XX PF 06-DEC-2001; 2001WO-US046587.

XX PR 06-DEC-2000; 2000US-0251892P.

XX PA (NEUR-) NEURALAB LTD.

XX PY (AMHP) WYETH.

XX PI Basi G, Saldanha J, Yednock T;

XX DR WPI; 2002-519658/55.

XX N-PSDB; ABS59426.

XX PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.

XX PS Claim 67; Fig 1; 171pp; English.

XX CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful

CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
CC variable heavy (VH) chain protein of the invention
XX
SQ Sequence 132 AA;

Query Match 100.0%; Score 692; DB 5; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.3e-55;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMSPAQFLFLVLVWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNM 60
DB 1 MMSPAQFLFLVLVWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNM 60
QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIEADLGLYVCWQGTTHP 120
DB 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIEADLGLYVCWQGTTHP 120
QY 121 RTFGGGTKLEIK 132
DB 121 RTFGGGTKLEIK 132

RESULT 2
ADR88406
ID ADR88406 standard; protein; 132 AA.
AC ADR88406;
XX
DT 16-DEC-2004 (first entry)
XX
DE Murine 3D6 immunoglobulin light chain variable region SEQ ID NO:2.
XX
KW 3D6; light chain variable region; immunoglobulin;
KW complementarity determining region; CDR; 10D5; variable framework region;
KW neuroprotective; neurotropic; gene therapy; amyloidogenic disease;
KW Alzheimer's disease.
XX
OS Mus musculus.

Key Location/Qualifiers
FT Peptide 1..20 /label= signal peptide
FT Protein 21..132
FT /label= mature protein
XX
PN WO2004080419-A2.
XX
PD 23-SEP-2004.
XX
PF 12-MAR-2004; 2004WO-US0007503.
XX
PR 12-MAR-2003; 2003US-00388389.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha JW, Yednock T;
XX
DR WPI; 2004-668880/65.
DR N-PSDB; ADR88405.

PT New humanized antibodies that recognize beta amyloid peptides, useful for
PT preventing or treating amyloidogenic diseases, such as Alzheimer's
PT disease.

PS Claim 1; SEQ ID NO 2; 176pp; English.
XX
XX The invention relates to a novel humanised immunoglobulin light or heavy
CC chain. The humanised immunoglobulin light or heavy chain comprises:
CC variable region complementarity determining regions (CDR's) from the 3D6
CC immunoglobulin light chain variable region sequence of 132 amino acids
CC fully defined in the specification (ADR88406), or heavy chain variable

CC region sequence of 138 amino acids fully defined in the specification
CC (ADR88406); or from the 10D5 immunoglobulin light chain variable region
CC sequence of 131 amino acids given in the specification (ADR88418) or
CC heavy chain variable region sequence of 142 amino acids fully defined in
CC the specification (ADR88420); and a variable framework region from a
CC human acceptor immunoglobulin light or heavy chain sequence, provided
CC that at least one framework residue is substituted with the corresponding
CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
CC variable region sequence, where the framework residue is a residue that
CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
CC -interacting residue or a residue participating in the VL-VH interface.
CC An antibody of the invention has neuroprotective and neurotropic activity,
CC and may have a use in gene therapy. The composition and methods are
CC useful for preventing or treating an amyloidogenic disease, such as
CC Alzheimer's disease. The variable region sequence is useful in producing
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
CC chain, or its domain. The present sequence represents the murine 3D6
CC immunoglobulin light chain variable region.

XX
SQ Sequence 132 AA;

Query Match 100.0%; Score 692; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.3e-55;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLVWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNM 60
DB 1 MMSPAQFLFLVLVWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNM 60
QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIEADLGLYVCWQGTTHP 120
DB 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIEADLGLYVCWQGTTHP 120
QY 121 RTFGGGTKLEIK 132
DB 121 RTFGGGTKLEIK 132

RESULT 3
ADM72033
ID ADM72033 standard; protein; 238 AA.
XX
AC ADM72033;
XX
DT 03-JUN-2004 (first entry)
XX
DE Chimeric mouse-human antibody M3C11 light chain.
XX
KW GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;
KW cytosstatic; M3C11.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN WO2004022739-A1.
XX
PD 18-MAR-2004.
XX
PF 04-SEP-2003; 2003WO-JP011318.
XX
PR 04-SEP-2002; 2002WO-JP008999.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;
XX
DR WPI; 2004-269573/25.
DR N-PSDB; ADM72032.
XX
PT Antibody against the N terminus of glypican 3 (GPC3) causes cell
PT disruption and is useful as an anticancer agent.
XX

PS Example 4; SEQ ID NO 18; 122pp; Japanese.

CC The invention relates to an antibody against the N terminus of glypican 3 (GPC3). The antibody can be used for causing cell disruption and can be used as an anti-cancer agent. The present sequence represents a chimeric mouse-human antibody M3C11 light chain.

XX Sequence 238 AA;

Query Match 94.7%; Score 655; DB 8; Length 238;
Best Local Similarity 94.7%; Pred. No. 2.8e-51;
Matches 124; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 MSPAQFLFLVLWIRENGYVMTQPTLTVITICQPASISCKSSQSLDSDGKTYLNWL 61
DB 1 MSPAQFLFLVLWIRENGYVMTQPTLTVITICQPASISCKSSQSLDSDGKTYLNWL 60

QY 62 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEARDLGLYYCWOQTTHPPR 121
DB 61 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEARDLGLYYCWOQTTHPPR 120

QY 122 TFGGCTKLEIK 132
DB 121 TFGACTKLEIK 131

RESULT 4

ADP45549
ID ADP45549 standard; protein; 238 AA.

AC ADP45549;

DT 09-SEP-2004 (first entry)

DE Mouse binding molecule 11C7 light chain SEQ ID NO:3.

XX binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;

KW nerve repair; neuroprotective; gene therapy;

KW central nervous system injury; CNS injury; neurodegenerative disorder;

KW mouse; antibody.

XX Mus musculus.

XX WO2004052932-A2.

XX 24-JUN-2004.

XX 09-DEC-2003; 2003WO-EP013960.

XX 10-DEC-2002; 2002GB-00028832.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS PHARMA GMBH.

XX (UYZU-) UNIV ZUERICH.

XX Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;

XX Zurini M;

XX WPI; 2004-468818/44.

XX New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.

PS Claim 9; SEQ ID NO 3; 121pp; English.

XX The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 100nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases

CC associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence represents a mouse binding molecule 11C7 light chain, which is used in the exemplification of the present invention.

XX Sequence 238 AA;

Query Match 94.4%; Score 653; DB 8; Length 238;
Best Local Similarity 93.9%; Pred. No. 4.2e-51;
Matches 123; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 MSPAQFLFLVLWIRENGYVMTQPTLTVITICQPASISCKSSQSLDSDGKTYLNWL 61
DB 1 MSPAQFLFLVLWIRENGYVMTQPTLTVITICQPASISCKSSQSLDSDGKTYLNWL 60

QY 62 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEARDLGLYYCWOQTTHPPR 121
DB 61 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEARDLGLYYCWOQTTHPPR 120

QY 122 TFGGCTKLEIK 132
DB 121 TFGGCTKLEIK 131

RESULT 5

ABB79729
ID ABB79729 standard; protein; 135 AA.

AC ABB79729;

DT 29-OCT-2002 (first entry)

DE Anti-Streptococcus mutans surface antigen MAB SWLA3 VL.

XX Streptococcus mutans; monoclonal antibody; MAB; mouse; chimeric antibody; antibody; anticaries; transgenic plant; transgenic animal; caries; immunotherapy; therapy.

XX Mus musculus.

XX US2002068066-A1.

XX 06-JUN-2002.

XX 15-JUN-2001; 2001US-00881823.

XX 20-AUG-1999; 99US-00378577.

XX (SHIW/) SHI W.

XX (MORR/) MORRISON S L.

XX (TRIN/) TRINH K.

XX (WIMS/) WIMS L.

XX (CHEN/) CHEN L.

XX (ANDE/) ANDERSON M H.

XX Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;

XX WPI; 2002-565838/60.

XX N-PSDB; ABN84610.

XX Treatment and prevention of dental caries in mammals, in particular humans by orally administering genetically engineered or purified antibodies that bind to surface antigens of carcinogenic organisms.

PS Claim 13; Fig 3A; 30pp; English.

XX The present sequence is the protein sequence of the light chain variable region (VL) of the murine monoclonal antibody SWLA3 (IgG), which binds specifically to the surface antigens of cariogenic type c Streptococcus mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC HB 12558) hybridoma cells. In an example from the invention, chimeric

CC monoclonal antibody TEFE was produced comprising SWLA3 variable regions
CC and human antibody constant regions. Such chimeric monoclonal antibodies
CC can be used to prevent or treat dental caries in humans. The antibodies
CC engage the effector apparatus of the human immune system when they bind
CC cariogenic organisms, resulting in their destruction. The chimeric
CC antibodies may be produced in edible plants, in transgenic animals, or in
CC chicken eggs for oral ingestion
XX
XX Sequence 135 AA;

Query Match 93.9%; Score 650; DB 5; Length 135;
Best Local Similarity 93.2%; Pred. No. 4.2e-51;
Matches 123; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 MMSPAQFLFLVLWIRETNGVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
DB 1 MMSPAQFLFLVLWIRETNGVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTTHP 120
DB 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTTHP 120
QY 121 RTFGGSKLEIK 132
DB 121 RTFGAGTKLELK 132

RESULT 6
ABF58274
ID ABP58274 standard; protein; 239 AA.
AC ABP58274;
DT 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
DE Humanised 3D6 antibody light chain.
XX
XX Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
KW human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
XX Mus sp.
OS Homo sapiens.
OS Chimeric.

Key Location/Qualifiers
FT Peptide 1..20 /label= Signal_peptide
FT Protein 21..239 /label= Mature_peptide
FT /note= "the mature light chain is claimed in Claim 5"
FT Region 21..133 /note= "light chain variable region, claimed in Claim 4"
FT Region 44..59 /note= "CDR1"
FT Region 75..81 /note= "CDR2"
FT Region 114..122 /note= "CDR3"

WO200288306-A2.
XX
XX
PD 07-NOV-2002.
XX
XX 26-APR-2002; 2002WO-US011853.
XX
XX 30-APR-2001; 2001US-0287539P.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Teurushita N, Vasquez M;

DR WPI; 2003-183835/18.
XX N-PSDB; ABZ24632, ABZ24634.
XX
XX New humanized forms of mouse 3D6 antibodies, useful for treating Down's
PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta
PT plaque in the brain.
XX
XX Disclosure; Page 12-13; 54pp; English.

XX
XX The present sequence is that of a preferred light chain of a humanised
CC antibody of the present invention. In the variable region of this
CC sequence, the complementarity determining regions (CDRs) originate from
CC murine monoclonal antibody 3D6 and the framework region from human
CC germline V_K segment DPK19 and J segment Jk4. Novel humanised antibodies
CC of the invention have CDRs from 3D6 and human framework sequences. These
CC humanised antibodies have binding affinities (affinity and epitope
CC location) approximately the same as those of the mouse 3D6 antibody. The
CC invention includes antibodies, single chain antibodies, and their
CC fragments, as well as nucleotide sequences, vectors, transformed host
CC cells, and methods of using the humanised antibody to treat, prevent,
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC OS field)
XX

Sequence 239 AA;

Query Match 93.1%; Score 644; DB 6; Length 239;
Best Local Similarity 90.9%; Pred. No. 2.8e-50;
Matches 120; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
DB 1 MMSPAQFLFLVLWIRETNGVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTTHP 120
DB 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTTHP 120
QY 121 RTFGGSKLEIK 132
DB 121 RTFGGSKVEIK 132

RESULT 7
AAR12361
ID AAR12361 standard; protein; 132 AA.

AC AAR12361;
XX
XX 25-MAR-2003 (revised)
DT 15-AUG-1991 (first entry)
DE Light (kappa) chain variable region of murine 4D12 immunoglobulin.
XX Chimeric antibodies; immunoconjugates; HIV; AIDS.

Mus musculus.

XX
XX WO9107493-A.
XX
XX 30-MAY-1991.
XX
XX 13-NOV-1989; 89US-00433730.
XX
XX 13-NOV-1989; 89US-00433730.
XX
XX (XOMA) XOMA CORP.
XX (GRC) GREEN CROSS CORP.

PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;

XX WPI; 1991-178105/24.
 DR N-ESDB; AAQ12063.
 XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV
 PT -1 antigen from sample.
 PT
 XX Disclosure; Fig 18; 107pp; English.
 PS This is the light (kappa) - chain variable (V) region of a mouse
 CC monoclonal antibody (Mab), 4D12, and is specific for an HIV-1 viral
 CC antigen. It is used in the construction of a chimeric Mab comprising
 CC heavy and light chains having murine V regions and human C regions. The
 CC chimeric MABs are more effective than murine MAB 4D12 since they have an
 CC increased compatibility in humans. The heavy and light chain V-regions
 CC are joined by manipulating their respective joining (J) regions, to
 CC generate restriction enzyme recognition sites. The chimeric MABs can be
 CC used as immunoconjugates, in association with e.g. toxins for HIV
 CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
 CC 62. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
 CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 132 AA;
 Query Match 92.6%; Score 641; DB 2; Length 132;
 Best Local Similarity 90.9%; Pred. No. 2.7e-50;
 Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MMSPAQFLFLVLVWIRETNGVVMVTQPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
 Db 1 MMSPAQFLFLVLVWIRETNGVVMVTQPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
 Qy 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRIRAEADLGLYYCQGTTHP 120
 Db 61 FLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRIRAEADLGLYYCQGTTHP 120
 Qy 121 RTFGGKLEIK 132
 Db 121 ITFGAGTKLEIR 132
 RESULT 8
 ADO00819 Antibody JRF/cabeta40/10 light chain variable region, SEQ ID 6.
 AC ADO00819 standard; protein; 133 AA.
 XX
 XX ADO00819;
 DT 01-JUL-2004 (first entry)
 DE Antibody JRF/cabeta40/10 light chain variable region, SEQ ID 6.
 XX Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;
 KW beta-amyloid-related disease; Alzheimer's disease; Abeta secretase;
 KW cleavage site; immunogen; murine; antibody; light chain; variable region;
 KW JRF/cabeta40/10.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 44..59
 FT /note= "CDR1"
 FT Domain 75..81
 FT /note= "CDR2"
 FT Domain 114..122
 FT /note= "CDR3"
 XX
 FN WO2004029629-A1.
 XX
 PD 08-APR-2004.
 PP 27-SEP-2002; 2002WO-EP011062.
 XX
 PR 27-SEP-2002; 2002WO-EP011062.

XX (JANC) JANSSEN PHARM NV.
 XX Mercken MH, Vandermeeren MMPP;
 PI WPI; 2004-316180/29.
 DR
 XX New N-11 truncated amyloid-beta monoclonal antibodies specific for human
 PT Amyloid-beta 11 N-terminal site (A-beta1-x peptides), useful for
 PT diagnosing or treating beta-amyloid-related diseases e.g. Alzheimer's
 PT disease.
 XX Disclosure; SEQ ID NO 6; 42pp; English.
 PS
 CC The present invention relates to an antibody expressed by the hybridoma
 CC cells J&JPRD/habetall1 and J&JPRD/habetall1/2, which is capable of
 CC specifically recognizing human Amyloid-beta 11 N-terminal site (i.e.,
 CC Abeta1-x peptides). The antibody is useful for diagnosing beta-amyloid-
 CC related diseases. It is particularly useful for prognosing and monitoring
 CC response to therapy of Alzheimer's disease and other beta-amyloid related
 CC diseases and in passive immunization as a method for treating such
 CC diseases. A humanized form of the antibody is useful for manufacturing a
 CC medicament for treating, preventing or reversing cognitive decline in
 CC clinical or pre-clinical Alzheimer's Disease, Down's syndrome, Hereditary
 CC Cerebral Hemorrhage with Amyloidosis of the Dutch-Type, cerebral amyloid
 CC angiopathy or other beta-amyloid-related diseases, or to inhibit the
 CC formation of amyloid plaques or the effects of toxic soluble Amyloid-beta
 CC ; species in humans. It can also be used in assay systems such as
 CC competitive methods and nephelometry. The present sequence was used to
 CC illustrate the invention.
 XX
 SQ Sequence 133 AA;
 Query Match 92.6%; Score 641; DB 8; Length 133;
 Best Local Similarity 91.7%; Pred. No. 2.7e-50;
 Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MMSPAQFLFLVLVWIRETNGVVMVTQPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
 Db 1 MMSPAQFLFLVLVWIRETNGVVMVTQPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
 Qy 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRIRAEADLGLYYCQGTTHP 120
 Db 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRIRAEADLGLYYCQGTTHP 120
 Qy 121 RTFGGKLEIK 132
 Db 121 RTFGGKLEIK 132
 RESULT 9
 ADO43845
 ID ADO43845 standard; protein; 133 AA.
 XX
 AC ADO43845;
 XX
 DT 15-JUL-2004 (first entry)
 DE Light chain variable region of anti-amyloid-beta antibody.
 XX
 KW antibody; Amyloid-beta1-x peptide; BACE-1; amyloid-beta; beta-secretase;
 KW beta-amyloid precursor protein; beta-amyloid-related disease;
 KW Alzheimer's disease; vaccine; Down's syndrome;
 KW hereditary cerebral haemorrhage; amyloidosis;
 KW cerebral amyloid angiopathy; amyloid plaque.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 44..59
 FT /note= "CDR1"
 FT Region 75..81
 FT /note= "CDR2"

FT	Region	114. .122	
FT		/note= "CDR3"	
XX	WO2004029630-A1.		
PN			
XX	08-APR-2004.		
PD			
XX	09-SEP-2003; 2003WO-EP010092.		
PF			
XX	27-SEP-2002; 2002WO-EP011062.		
PR			
XX	(JANC) JANSSEN PHARM NV.		
PA			
XX	Mercken MH, Vandermeeren MMPP;		
PI			
XX	WPI; 2004-316181/29.		
DR			
XX	New N-11 truncated amyloid-beta monoclonal antibodies specific for human		
PT	Amyloid-beta 11-x peptides (A-beta11-x peptides), useful for diagnosing		
PT	or treating beta-amyloid-related diseases e.g., Alzheimer's disease.		
PT			
PS	Disclosure; Page 38-39; 50pp; English.		
XX			
CC	The specification describes a monoclonal antibody which specifically		
CC	recognizes human Amyloid-beta11-x peptides. These peptides result from		
CC	overexpression of BACE-1 which causes additional cleavage at the +11 site		
CC	of amyloid-beta, generating shorter fragments known as Amyloid-beta11-x		
CC	peptides. BACE-1 is the major beta-secretase required for cleavage of		
CC	beta-amyloid precursor protein. The antibody is useful for detecting the		
CC	presence of amyloid-beta peptides in a tissue or fluid sample and for		
CC	diagnosing beta-amyloid-related diseases. It is particularly useful for		
CC	prognosing and monitoring response to therapy of Alzheimer's disease and		
CC	other beta-amyloid related diseases and in passive immunization as a		
CC	method for treating such diseases. A humanized form of the antibody is		
CC	useful for manufacturing a medicament for treating, preventing or		
CC	reversing cognitive decline in clinical or pre-clinical Alzheimer's		
CC	Disease, Down's syndrome, Hereditary Cerebral Haemorrhage with		
CC	Amyloidosis of the Dutch-Type, cerebral amyloid angiopathy or other beta-		
CC	amyloid-related diseases, or to inhibit the formation of amyloid plaques		
CC	or the effects of toxic soluble Amyloid-beta species in humans. The		
CC	present sequence represents the light chain variable region of an		
CC	antibody that recognises amyloid-beta-40 and amyloid-beta11-x peptide		
CC	amyloid-beta11-40.		
XX			
XX	Sequence 133 AA;		
SQ			
Query Match 92.8%; Score 641; DB 8; Length 133;			
Best Local Similarity 91.7%; Pred. No. 2.7e-50;			
Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;			
QY	1	MMSPAQFLFLVLVIRETNGYVVMQTPTLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60	
Db	1	MMSPAQFLFLVLVIRETNGYVVMQTPTLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60	
QY	61	LLQRPQSQPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCQGTTHP 120	
Db	61	LLQRPQSQPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCQGTTHP 120	
QY	121	RTFGGQTKLEIK 132	
Db	121	RTFGGQTKLEIK 132	
RESULT 10			
ABG76925			
ID	ABG76925	standard; protein; 132 AA.	
XX			
AC	ABG76925;		
XX			
DT	05-NOV-2002	(first entry)	
XX			
DE	Humanised 3D6 light chain variable region #1.		
XX			
KW	Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;		
KW	variable region complementarity determining region; 3D6; 10D5;		
KW	variable framework region; amyloidogenic disease; Alzheimer's disease;		
KW	amyloid deposit; variable light chain; VU; variable heavy chain; VH;		
KW	notropic; neuroprotective; inhibitor of beta amyloid accumulation;		
KW	Abeta.		
XX			
OS	Homo sapiens.		
OS	Mus musculus.		
OS	Synthetic.		
XX			
PN	WO200246237-A2.		
XX			
PD	13-JUN-2002.		
XX			
PF	06-DEC-2001; 2001WO-US046587.		
XX			
PR	06-DEC-2000; 2000US-0251892P.		
XX			
PA	(NEUR-) NEURALAB LTD.		
PA	(AMHP) WYETH.		
XX			
PI	Basi G, Saldanha J, Yednock T;		
XX			
DR	WPI; 2002-519658/55.		
XX			
PT	Novel light/heavy chain of humanized immunoglobulin for treating		
PT	amyloidogenic disease, has 3D6/10D5 variable region complementarity		
PT	determining regions and variable framework region from human acceptor		
PT	immunoglobulin.		
XX			
PS	Claim 54; Page 154; 171pp; English.		
XX			
CC	The present invention relates to new humanized immunoglobulin (Ig) light		
CC	chain (LC) or heavy chain (HC) comprising variable region complementarity		
CC	determining regions from 3D6/10D5 Ig LC or HC variable region sequence,		
CC	and variable framework region from human acceptor Ig LC or HC sequence.		
CC	The invention is useful for preventing or treating an amyloidogenic		
CC	disease or Alzheimer's disease in a patient. The invention is also useful		
CC	for in vivo imaging amyloid deposits in a patient. The present amino acid		
CC	sequence represents a humanized 3D6 variable light (VL) chain or variable		
CC	heavy (VH) chain protein of the invention		
XX			
SQ	Sequence 132 AA;		
Query Match 92.5%; Score 640; DB 5; Length 132;			
Best Local Similarity 90.2%; Pred. No. 3.3e-50;			
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;			
QY	1	MMSPAQFLFLVLVIRETNGYVVMQTPTLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60	
Db	1	MMSPAQFLFLVLVIRETNGYVVMQTPTLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60	
QY	61	LLQRPQSQPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCQGTTHP 120	
Db	61	LLQRPQSQPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCQGTTHP 120	
QY	121	RTFGGQTKLEIK 132	
Db	121	RTFGGQTKLEIK 132	
RESULT 11			
ADR88409			
ID	ADR88409	standard; protein; 132 AA.	
XX			
AC	ADR88409;		
XX			
DT	16-DEC-2004	(first entry)	
XX			
DE	Humanised 3D6 immunoglobulin light chain variable region SEQ ID NO:5.		
XX			
KW	3D6; light chain variable region; immunoglobulin;		

KW complementarity determining region; CDR, 10D5; variable framework region;
KW neuroprotective; nootropic; gene therapy; amyloidogenic disease;
KW Alzheimer's disease.
OS Synthetic.

XX Key Location/Qualifiers
FH Peptide 1..20
FT /label= signal peptide
FT Protein 21..132
FT /label= mature protein

XX WO2004080419-A2.

XX 23-SEP-2004.

XX 12-MAR-2004; 2004WO-US007503.

XX 12-MAR-2003; 2003US-00388389.

XX (NEUR-) NEURALAB LTD.
XX (AMHP) WYETH.

XX Basi G, Saldanha JW, Yednock T;

XX WPI; 2004-668880/65.

XX New humanized antibodies that recognize beta amyloid peptides, useful for
XX preventing or treating amyloidogenic diseases, such as Alzheimer's
XX disease.

XX Claim 54; SEQ ID NO 5; 176pp; English.

XX The invention relates to a novel humanised immunoglobulin light or heavy
XX chain. The humanised immunoglobulin light or heavy chain comprises:
XX variable region complementarity determining regions (CDR's) from the 3D6
XX immunoglobulin light chain variable region sequence of 132 amino acids
XX fully defined in the specification (ADR88406), or heavy chain variable
XX region sequence of 138 amino acids fully defined in the specification
XX (ADR88408); or from the 10D5 immunoglobulin light chain variable region
XX sequence of 131 amino acids given in the specification (ADR88418) or
XX heavy chain variable region sequence of 142 amino acids fully defined in
XX the specification (ADR88420); and a variable framework region from a
XX human acceptor immunoglobulin light or heavy chain sequence, provided
XX that at least one framework residue is substituted with the corresponding
XX amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
XX variable region sequence, where the framework residue is a residue that
XX non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
XX -interacting residue or a residue participating in the VL-VH interface.
XX An antibody of the invention has neuroprotective and nootropic activity,
XX and may have a use in gene therapy. The composition and methods are
XX useful for preventing or treating an amyloidogenic disease, such as
XX Alzheimer's disease. The variable region sequence is useful in producing
XX a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
XX chain, or its domain. The present sequence represents a humanised
XX immunoglobulin of the invention.

XX Sequence 132 AA;

Query Match 92.5%; Score 640; DB 8; Length 132;
Best Local Similarity 90.2%; Pred. NO. 3.3e-50;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 MMSPAQLFLVLVIRETNGVYVMTQTPLTSLVITGQPASISCKSSQSLSDSGKTYLW 60
Db 1 MMSPAQLFLVLVIRETNGVYVMTQTPLTSLVITGQPASISCKSSQSLSDSGKTYLW 60

QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRIAEADGLGYCQGHFP 120
Db 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRIAEADGLGYCQGHFP 120

QY 121 RTFGGKLEIK 132

|||||

Db 121 RTFGGKLEIK 132
RESULT 12
AAR12239
ID AAR12239 standard; protein; 131 AA.
XX AAR12239;
AC AAR12239;
XX 25-MAR-2003 (revised)
DT 19-AUG-1991 (first entry)
XX Mouse Mab 4D12 L chain V region.
DE HIV-1; chimera.
XX Mus sp.
OS Mus sp.
XX WO9107494-A.
XX 30-MAY-1991.
XX 13-NOV-1989; 89US-00433703.
XX 13-NOV-1989; 89US-00433703.
XX (XOMA) XOMA CORP.
XX (GREC) GREEN CROSS CORP.
XX (ZOMA-) ZOMA CORP.

XX Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;

XX WPI; 1991-178106/24.

XX N-PSDB; AAQ12019.

XX New chimeric mouse human antibodies - used in treatment, diagnosis and
XX prophylaxis of HIV infections.
XX Disclosure; Fig 18; 108pp; English.
XX The mouse VL gene product may be used to produce chimeric mouse- human
XX Abs against HIV-1 comprising human Ig constant regions and murine
XX variable regions. These novel sequence are useful in treatment, diagnosis
XX and prophylaxis of HIV infections, and may be produced by a bacterial,
XX yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
XX PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 131 AA;

Query Match 92.3%; Score 639; DB 2; Length 131;
Best Local Similarity 91.6%; Pred. No. 4e-50;
Matches 120; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MMSPAQLFLVLVIRETNGVYVMTQTPLTSLVITGQPASISCKSSQSLSDSGKTYLW 60
Db 1 MMSPAQLFLVLVIRETNGVYVMTQTPLTSLVITGQPASISCKSSQSLSDSGKTYLW 60

QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRIAEADGLGYCQGHFP 120
Db 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRIAEADGLGYCQGHFP 120

QY 121 RTFGGKLEIK 131

|||||

Db 121 RTFGGKLEIK 131

|||||

QY 121 RTFGGKLEIK 131

|||||

Db 121 RTFGGKLEIK 131

|||||

QY 121 RTFGGKLEIK 131

|||||

Db 121 RTFGGKLEIK 131

|||||

QY 121 RTFGGKLEIK 131

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Db 121 RTFGGKLEIK 131

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QY 121 RTFGGKLEIK 131

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XX DE Mouse antibody 3D8 light chain variable region.
XX DE
XX DE
XX KW T-cell receptor; cytostatic; dermatological; neuroprotective;
XX KW immunostimulant; GD3; ganglioside antigen; MB3.6; FSMA; tumour; 3D8; 4D4;
XX KW 3E11; prostate-specific membrane antigen; zeta signalling chain;
XX KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
XX KW small cell lung cancer; light chain variable region; mouse.
XX OS
XX OS Mus sp.
XX PN US2002132983-A1.
XX PD 19-SEP-2002.
XX PF 10-DEC-2001; 2001US-00006773.
XX PR 30-NOV-2000; 2000US-0250087P.
XX PR 30-NOV-2000; 2000US-0250089P.
XX PA (JUNG/) JUNGHANS R P.
XX PI Junghans RP;
XX PX WPI; 2003-208946/20.
XX DR N-PSDB; ABX16570.
XX PT New chimeric molecule useful in treating patients with disorders, such as
XX PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
XX PT comprises GD3 and/or PSMA binding domains of antibody.
XX PS Disclosure; Page 13; 35pp; English.
XX CC The invention relates to a chimeric molecule comprising the GD3
XX CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
XX CC variable gene sequences, or the FSMA (prostate-specific membrane antigen)
XX CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
XX CC sequences, the zeta signalling chain of the T cell receptor and an
XX CC intervening CD8alpha hinge in which cysteine residues have been mutated.
XX CC The chimeric molecules expressed in T cells or NK cells or other
XX CC effector cells are useful in treating patients with cancers expressing
XX CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
XX CC and/or together with each other or with heterologous constructs to engage
XX CC additional stimulatory and functional properties of the effector cells to
XX CC enhance the antitumour therapeutic efficacy (claimed). They are
XX CC particularly useful in disorders including melanoma, neuroendocrine
XX CC tumours and prostate and small cell lung cancer. The present sequence
XX CC represents the mouse antibody 3D8 light chain variable region
XX SQ Sequence 132 AA;
XX Query Match 91.9%; Score 636; DB 6; Length 132;
XX Best Local Similarity 93.9%; Pred. No. 7.6e-50;
XX Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 MSPAQFLFLVLWIRETNGYVVMQTPTLTSLVTIGQPASISCKSSQSLSDSGKTYLNL 61
DB 1 MSPAQFLFLVLWIRETNGYVVMQTPTLTSLVTIGQPASISCKSSQSLSDSGKTYLNL 60
QY 62 LQPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTTHPP 121
DB 61 LQPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTTHPP 120
QY 122 TFGGGTKLEIK 132
DB 121 TFGGGTKLEIK 131
RESULT 14
ID ABG76931
XX ABG76931 standard; protein; 132 AA.
XX AC ABG76931;

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XX DT 05-NOV-2002 (first entry)
XX DE Humanised 3D6 light chain variable region #2.
XX DE
XX KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
XX KW variable region complementarity determining region; 3D6; 10D5;
XX KW variable framework region; amyloidogenic disease; Alzheimer's disease;
XX KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
XX KW neotropic; neuroprotective; inhibitor of beta amyloid accumulation;
XX KW Abeta.
XX OS Homo sapiens.
XX OS Mus musculus.
XX OS Synthetic.
XX PN WO200246237-A2.
XX PD 13-JUN-2002.
XX PX 06-DEC-2001; 2001WO-US046587.
XX PR 06-DEC-2000; 2000US-0251892P.
XX PA (NEUR-) NEURALAB LTD.
XX PA (AMHP ) WYETH.
XX PI Basi G, Saldanha J, Yednock T;
XX PX WPI; 2002-519658/55.
XX PT Novel light/heavy chain of humanized immunoglobulin for treating
XX PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
XX PT determining regions and variable framework region from human acceptor
XX PS immunoglobulin.
XX PS Claim 55; Page 157; 171pp; English.
XX CC The present invention relates to new humanized immunoglobulin (Ig) light
XX CC chain (LC) or heavy chain (HC) comprising variable region complementarity
XX CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
XX CC and variable framework region from human acceptor Ig LC or HC sequence.
XX CC The invention is useful for preventing or treating an amyloidogenic
XX CC disease or Alzheimer's disease in a patient. The invention is also useful
XX CC for in vivo imaging amyloid deposits in a patient. The present amino acid
XX CC sequence represents a humanized 3D6 variable light (VL) chain or variable
XX CC heavy (VH) chain protein of the invention
XX SQ Sequence 132 AA;
XX Query Match 91.0%; Score 630; DB 5; Length 132;
XX Best Local Similarity 89.4%; Pred. No. 2.7e-49;
XX Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
QY 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTSLVTIGQPASISCKSSQSLSDSGKTYLNL 60
DB 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTSLVTIGQPASISCKSSQSLSDSGKTYLNL 60
QY 61 LLQPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTTHPP 120
DB 61 LLQPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTTHPP 120
QY 121 RTFGGGTKLEIK 132
DB 121 RTFGGGTKLEIK 132
RESULT 15
ID ADR88415
XX ADR88415 standard; protein; 132 AA.
XX AC ADR88415;
XX AC

```

DT 16-DEC-2004 (first entry)
DE Humanised 3D6 immunoglobulin light chain variable region SEQ ID NO:11.
XX
XX 3D6; light chain variable region; immunoglobulin;
KW complementarity determining region; CDR, 10D5; variable framework region;
KW neuroprotective; nootropic; gene therapy; amyloidogenic disease;
KW Alzheimer's disease.
XX
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
FT Peptide 1..20
FT /label= signal peptide
FT Protein 21..132
FT /label= mature protein
XX
XX WO2004080419-A2.
XX
XX 23-SEP-2004.
XX
XX 12-MAR-2004; 2004WO-US007503.
XX
XX 12-MAR-2003; 2003US-00388389.
XX (NEUR-) NEURALAB LTD.
XX (AMHP) WYETH.
XX
XX Basi G, Saldanha JW, Yednock T;
XX WPI; 2004-668880/65.
XX
XX New humanized antibodies that recognize beta amyloid peptides, useful for
XX preventing or treating amyloidogenic diseases, such as Alzheimer's
XX disease.
XX
XX Claim 55; SEQ ID NO 11; 176pp; English.
XX
XX The invention relates to a novel humanised immunoglobulin light or heavy
XX chain. The humanised immunoglobulin light or heavy chain comprises:
XX variable region complementarity determining regions (CDR's) from the 3D6
XX immunoglobulin light chain variable region sequence of 132 amino acids
XX fully defined in the specification (ADR88406), or heavy chain variable
XX region sequence of 138 amino acids fully defined in the specification
XX (ADR88408); or from the 10D5 immunoglobulin light chain variable region
XX sequence of 131 amino acids given in the specification (ADR88418) or
XX heavy chain variable region sequence of 142 amino acids fully defined in
XX the specification (ADR88420); and a variable framework region from a
XX human acceptor immunoglobulin light or heavy chain sequence, provided
XX that at least one framework residue is substituted with the corresponding
XX amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
XX variable region sequence, where the framework residue is a residue that
XX non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
XX -interacting residue or a residue participating in the VL-VH interface.
XX An antibody of the invention has neuroprotective and nootropic activity,
XX and may have a use in gene therapy. The composition and methods are
XX useful for preventing or treating an amyloidogenic disease, such as
XX Alzheimer's disease. The variable region sequence is useful in producing
XX a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
XX chain, or its domain. The present sequence represents a humanised
XX immunoglobulin of the invention.
XX
XX Sequence 132 AA;
XX
XX Query Match 91.0%; Score 630; DB 8; Length 132;
XX Best Local Similarity 89.4%; Pred. NO. 2.7e-49;
XX Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 MMSPAQFLFLVLVLTRETNQVVMQTPLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60
XX
XX 1 MMSPAQFLFLVLVLTRETNQVVMQTPLSLPVTGPEPASISCKSSQSLDSDGKTYLNW 60
XX
XX 61 LLQRPQGSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEADVGVIYCWQGTTHFP 120

Db 61 LLQRPQGSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEADVGVIYCWQGTTHFP 120
Oy 121 RTFGGQTKLEIK 132
Db 121 RTFGGQTKVEIK 132
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Job time : 89 secs

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OM protein - protein search, using sw model

Run on: September 26, 2005, 06:27:34 ; Search time 25 Seconds
(without alignments)
508.025 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MWSPAQLFLVLVIRETNG.....CWQGTFFRPTGGGKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	98.0	132	2 C32513	Ig kappa chain pre
2	587	84.8	131	2 S31577	Ig kappa chain - m
3	566	81.8	113	2 P30560	Ig kappa chain v r
4	554	80.1	112	2 A5491	proteolytic antibo
5	548	79.2	112	2 A36259	Ig kappa chain v r
6	547	79.0	111	2 S20709	Ig kappa chain v r
7	536	77.5	112	2 P40273	Ig kappa chain v r
8	516	74.6	133	2 S42611	HUNVK protein prec
9	515	74.4	101	2 A33730	Ig kappa chain v r
10	515	74.4	133	2 S23230	Ig kappa chain pre
11	513	74.1	142	2 S22902	Ig kappa chain v r
12	512	74.0	133	2 S40324	Ig kappa chain v r
13	508	73.4	133	1 K2HURP	Ig kappa chain pre
14	502.5	72.6	140	2 S22658	Ig kappa chain pre
15	496	71.7	133	1 A24452	Ig kappa chain pre
16	491	71.0	132	2 S40322	Ig kappa chain - h
17	485	70.1	103	2 PH1055	Ig light chain v r
18	476	68.8	91	2 S42186	Ig kappa chain v r
19	473	68.4	120	2 S42268	Ig kappa chain v r
20	473	68.4	120	2 S42267	Ig kappa chain v r
21	470	67.9	131	2 S09259	Ig kappa chain pre
22	466	67.3	103	2 PH1056	Ig light chain v r
23	463	66.9	126	2 S40312	Ig kappa chain - h
24	463	66.9	131	2 D29380	Ig kappa chain pre
25	462.5	66.8	131	2 S40355	Ig kappa chain - h
26	462	66.8	132	2 S26882	Ig kappa chain v r
27	461.5	66.7	114	2 S49572	Ig kappa chain pre
28	460	66.5	118	2 S40374	Ig kappa chain - h
29	458.5	66.3	114	2 B49002	Ig kappa chain v r

RESULT 1
C32513
Ig kappa chain precursor V region (BXW14) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: C32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94689; MUID:88331394; PMID:3138286
A:Accession: C32513
A:Molecule type: DNA
A:Residues: 1-132 <KOF>
A:Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMW>

Query Match 98.0%; Score 678; DB 2; Length 132;
Best Local Similarity 97.7%; Pred. No. 1.6e-51;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MWSPAQLFLVLVIRETNGYVMTQTPTLTLSVTIGQPASISCKSSQSLSDGKTYLW 60
Db 1 MWSPAQLFLVLVIRETNGYVMTQTPTLTLSVTIGQPASISCKSSQSLSDGKTYLW 60
Qy 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTIKISRIEADTLGLYYCWQGTTHP 120
Db 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTIKISRIEADTLGLYYCWQGTTHP 120
Qy 121 RTFGGKLEIK 132
Db 121 RTFGGKLEIK 132

RESULT 2
S31577
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S31577
R:Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.
submitted to the EMBL Data Library, January 1993
A:Description: Immunoglobulin variable heavy and light chain cDNA sequences for two antic
A:Reference number: S31577
A:Accession: S31577
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <REC>
A:Cross-references: EMBL:Z19575; NID:g53983; PIDN:CAA79627.1; PID:g53984
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

ALIGNMENTS


```
RESULT 7
PL0273
Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: PL0273
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0273
A:Molecule type: mRNA
A:Residues: 1-112 <SHL>
A:Cross-references: UNIPROT:Q8K0F8
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-95/Domain: immunoglobulin homology <IMM>
F:24-39/Region: complementarity-determining 1
F:40-54/Region: framework 2
F:55-61/Region: complementarity-determining 2
F:62-93/Region: framework 3
F:94-102/Region: complementarity-determining 3
F:103-112/Region: framework 4

Query Match 77.5%; Score 536; DB 2; Length 112;
Best Local Similarity 93.7%; Pred. No. 2.3e-39; Mismatches 3; Indels 0; Gaps 0;
Matches 104; Conservative 3;

Qy 22 VVMTQTPLTSLVITIGQPASISCKSSQSLSDSGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQTPLTSLVITIGQPASISCKSSQSLLYRNGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYCWQGTTHPPFRTGGGKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYVCVQGTTHPPFRTGGGKLEIK 112

RESULT 8
S42611
HUNK protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42611
R:Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.
J. Neuroimmunol. 36, 29-39, 1992
A:Title: DNA sequence analysis and comparison of the variable heavy and light chain regi
A:Reference number: S42610; MUID:92138794; PMID:1370957
A:Accession: S42611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <SPA>
A:Cross-references: EMBL:X54137; NID:g433889; PIDN:CAA38072.1; PID:g433890
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 516; DB 2; Length 133;
Best Local Similarity 74.0%; Pred. No. 1.4e-37;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQLFLVLVLTRETNGYVVMVTQTPLTSLVITIGQPASISCKSSQSLSDSGKTYLNW 60
Db 1 MRLPAQLGLLMLWPGSGGDVVMVTQSPLSLPTVLGQPASISCRSSQSLVSDGNTYLNW 60

Qy 61 LLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYCWQGTTHP 120
Db 61 FQRPQSPKRLIYKVNRDGSVPDRFSGSGSGTDFTLKISRVEADVGIYCYCQGAHP 120

Qy 121 RTFGGKLEIK 131
Db 121 LTFGGGKVEI 131
```

```
RESULT 9
A33730
Ig kappa chain V region (1.60) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C:Accession: A33730
R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A:Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A:Reference number: A33730; MUID:89367325; PMID:2505260
A:Accession: A33730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <LAW>
A:Cross-references: GB:M25996; NID:g197109; PIDN:AAA38911.1; PID:g197110
A:Note: the authors translated the codon CGC for residue 51 as Leu, and TTG for residue 8
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 515; DB 2; Length 101;
Best Local Similarity 98.0%; Pred. No. 1.3e-37;
Matches 97; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVITIGQPASISCKSSQSLSDSGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQTPLTSLVITIGQPASISCKSSQSLSDSGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYCWQGTTHP 120
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYVCWQGTTHP 100

RESULT 10
S23230
Ig kappa chain precursor V-J region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S23230
R:Kennedy, M.A.
J. Exp. Med. 173, 1033-1036, 1991
A:Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and lig
A:Reference number: S23230; MUID:91178438; PMID:1840606
A:Accession: S23230
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <KEN>
A:Cross-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 515; DB 2; Length 133;
Best Local Similarity 74.2%; Pred. No. 1.7e-37;
Matches 98; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQLFLVLVLTRETNGYVVMVTQTPLTSLVITIGQPASISCKSSQSLSDSGKTYLNW 60
Db 1 MRLPAQLGLLMLWPGSGGDVVMVTQSPLSLPTVLGQPASISCRSSQSLVSDGNTYLNW 60

Qy 61 LLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYCWQGTTHP 120
Db 61 FQRPQSPKRLIYKVNRDGSVPDRFSGSGSGTDFTLKISRVEADVGIYCYCQGTTHP 120

Qy 121 RTFGGKLEIK 132
Db 121 YTFGGKLEIK 132
```

```
RESULT 11
S22902
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S22902
R:Chastagner, P.; Theze, J.; Zouali, M.
Gene 101, 305-306, 1991
A:Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region us
A:Reference number: S22902; MUID:91276289; PMID:1905262
A:Accession: S22902
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-142 <CHA>
A:Cross-references: EMBL:X56510
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-126/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 513; DB 2; Length 142;
Best Local Similarity 74.0%; Pred. No. 2.7e-37;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNQYVMTQPLTSLVTICQPASISCKSSQSLSDSGKTYLNM 60
DB 12 MRLPAQLGLLMLWVPGSSGDVMTQPSLPTVLGQPASISCRSSQSLVHSDGNTYLNW 71

QY 61 LLQRPQSPKRLIYLVKLDGVPDRFTGSGSGTDTFLKISRIEADLGLIYCWQGTTHP 120
DB 72 FQORPQSPRLIYKVSNRDSGVPDRFSGSGTDTFLKISRIEADLGLIYCWQGTTHP 131

QY 121 RTFGGQTKLEI 131
DB 132 FTFGQGTTRLEI 142

RESULT 12
S40324
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40324
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-133 <KLE>
A:Cross-references: UNIPROT:Q8TCD0; EMBL:X72434
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-112/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 512; DB 2; Length 133;
Best Local Similarity 74.4%; Pred. No. 3.1e-37;
Matches 96; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 4 PAQFLFLVLWIRETNQYVMTQPLTSLVTICQPASISCKSSQSLSDSGKTYLNLQ 63
DB 1 PAQLGLLMLWVPGSSGDVLTQPSLPTVLGQPASISCRSSQSLVSDGKTYLWYQQ 60

QY 64 RPQSPKRLIYLVKLDGVPDRFTGSGSGTDTFLKISRIEADLGLIYCWQGTTHP 123
DB 61 RPQSPKRLIYKVSNRDSGVPDRFTGSGSGTDTFLKISRIEADLGLIYCWQGTTHP 120

QY 124 GGQTKLEIK 132
DB 121 GGQTKVEIK 129

RESULT 13
S22658
Ig kappa chain precursor V region (0-81VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C:Accession: S22658
R:Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 2601, 1992
A:Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-as
A:Reference number: S22657; MUID:92285150; PMID:1598223
A:Accession: S22658
A:Molecule type: mRNA
A:Residues: 1-140 <HIR>
A:Cross-references: UNIPROT:Q8TCD0; EMBL:X59135
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 72.6%; Score 502.5; DB 2; Length 140;
```

```
K2HURP
Ig kappa chain precursor V-II region (RPMI) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A01890
R:Klobeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A:Reference number: A93588; MUID:86041852; PMID:2997711
A:Accession: A01890
A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A:Cross-references: UNIPROT:P06310
A>Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-115/Domain: immunoglobulin homology <IMM>
F:44-59/Region: complementarity-determining 1
F:60-74/Region: framework 2
F:75-81/Region: complementarity-determining 2
F:82-113/Region: framework 3
F:114-122/Region: complementarity-determining 3
F:123-133/Region: framework 4
F:43-113/Disulfide bonds: #status predicted

Query Match 73.4%; Score 508; DB 1; Length 133;
Best Local Similarity 73.5%; Pred. No. 6.9e-37;
Matches 97; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNQYVMTQPLTSLVTICQPASISCKSSQSLSDSGKTYLNM 60
DB 1 MRLPAQLGLLMLWVPGSSGDVMTQPSLPTVLGQPASISCRSSQSLVSDGNTYLNW 60

QY 61 LLQRPQSPKRLIYLVKLDGVPDRFTGSGSGTDTFLKISRIEADLGLIYCWQGTTHP 120
DB 61 FQORPQSPRLIYKVSNRDSGVPDRFSGSGTDTFLKISRIEADLGLIYCWQGTTHS 120

QY 121 RTFGGQTKLEIK 132
DB 121 WTFGQGTKEIK 132

RESULT 14
S22658
Ig kappa chain precursor V region (0-81VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C:Accession: S22658
R:Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 2601, 1992
A:Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-as
A:Reference number: S22657; MUID:92285150; PMID:1598223
A:Accession: S22658
A:Molecule type: mRNA
A:Residues: 1-140 <HIR>
A:Cross-references: UNIPROT:Q8TCD0; EMBL:X59135
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 72.6%; Score 502.5; DB 2; Length 140;
```



```

Best Local Similarity 73.7%; Pred. No. 2.2e-36;
Matches 98; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 MMSPAQFLFLVLWIRETVGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MRLPAQLGLLMLWVFGSGDVVMTQSPLSLPTVLGQPASISCRSSQSLVHSDGNTYLNW 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 LLQRGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEADGLVYCMQGTTHP- 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 FQQRFGQSPRLIYRVSNRDGVPDRFTGSGSGTDFTLKISRVEADGLVYCMQGTTHWS 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 120 PRTFGGGKLEIK 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 PITFGQGTKEIK 133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
A24452
Ig kappa chain precursor V-II region (RPMI 6410) - human
C:Species: Homo sapiens (man)
C:Date: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C:Accession: A24452
R:Weir, L.; Leder, P.
Nucleic Acids Res. 14, 3957-3970, 1986
A:Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.
A:Reference number: A24452; MOID:86232631; PMID:3086847
A:Accession: A24452
A:Molecule type: DNA
A:Residues: 1-133 <WEI>
A:Cross-references: GB:M36859; NID:q185932; PIDN:AAA58920.1; PID:q185933
A:Note: this sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted

Query Match 71.7%; Score 496; DB 1; Length 133;
Best Local Similarity 72.7%; Pred. No. 7.4e-36;
Matches 96; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETVGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MRLPAQLGLLMLWVFGSGDVVMTQSPLSLPTVLGQPASISCRSSQSLVSDRNTYLNW 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 LLQRGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEADGLVYCMQGTTHP 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 FQQRFGQSPRLIYKVSNRDGVPDRFTGSGSGTDFTLKISRVEADGVVYCMQGTTHWS 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 RTFGGKLEIK 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 WTFGQGTKEIK 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: September 26, 2005, 07:18:27
Job time : 26 secs

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OM protein - protein search, using sw model

Run on: September 26, 2005, 06:29:58 ; Search time 28 Seconds
(without alignments)
351.917 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQGTHTPRTGGGKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	93.8	131	4	US-09-647-468-163
2	646	93.4	131	4	US-09-647-468-164
3	606	87.6	142	4	US-09-840-459-102
4	606	87.6	142	4	US-09-497-625A-102
5	571	82.5	113	4	US-09-698-705-7
6	571	82.5	218	4	US-09-698-705-12
7	562	81.2	353	4	US-09-203-958A-4
8	560	80.9	112	4	US-09-809-739-11
9	560	80.9	112	4	US-09-840-459-9
10	560	80.9	112	4	US-09-497-625A-9
11	559	80.8	257	4	US-09-419-788-113
12	559	80.8	112	4	US-09-647-468-149
13	559	80.8	112	4	US-09-647-468-150
14	556	80.3	112	4	US-09-840-459-54
15	556	80.3	112	4	US-09-497-625A-54
16	548	79.2	112	2	US-08-678-194-6
17	548	79.2	112	3	US-08-890-011-6
18	548	79.2	112	3	US-09-262-724-6
19	548	79.2	535	3	US-08-983-035A-38
20	538	77.7	112	4	US-09-809-739-16
21	538	77.7	112	4	US-09-840-459-14
22	538	77.7	112	4	US-09-497-625A-14
23	537	77.6	132	1	US-08-477-877B-91
24	537	77.6	132	2	US-08-472-281A-91
25	537	77.6	132	2	US-08-477-989B-91
26	533	77.0	112	4	US-09-809-739-17
27	533	77.0	112	4	US-09-840-459-15

28 533 77.0 112 4 US-09-497-625A-15 Sequence 15, Appl
29 530 76.6 112 4 US-09-809-739-15 Sequence 15, Appl
30 530 76.6 112 4 US-09-840-459-13 Sequence 13, Appl
31 530 76.6 112 4 US-09-497-625A-13 Sequence 13, Appl
32 527 76.2 114 4 US-09-840-459-106 Sequence 106, App
33 527 76.2 114 4 US-09-497-625A-106 Sequence 106, App
34 525 75.9 112 4 US-09-809-739-18 Sequence 18, Appl
35 525 75.9 112 4 US-09-840-459-107 Sequence 107, App
36 520 75.1 112 4 US-09-809-739-14 Sequence 14, Appl
37 520 75.1 112 4 US-09-840-459-12 Sequence 12, Appl
38 520 75.1 112 4 US-09-497-625A-12 Sequence 12, Appl
39 518 74.9 132 1 US-08-477-877B-84 Sequence 84, Appl
40 518 74.9 132 2 US-08-472-281A-84 Sequence 84, Appl
41 518 74.9 132 2 US-08-477-989B-84 Sequence 84, Appl
42 515 74.4 100 4 US-09-840-459-22 Sequence 22, Appl
43 515 74.4 100 4 US-09-497-625A-22 Sequence 22, Appl
44 515 74.4 135 1 US-08-259-372A-12 Sequence 12, Appl
45 515 74.4 135 1 US-08-468-671-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-647-468-163

; Sequence 163, Application US/09647468

; Patent No. 6677436

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; APPLICANT: ADACHI, HIDEKI

; APPLICANT: YASUTA, NAOKI

; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; FILE REFERENCE: 053466/0289

; CURRENT APPLICATION NUMBER: US/09/647,468

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: JP 10-91850

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 183

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 163

; LENGTH: 131

; TYPE: PRT

; ORGANISM: Mus sp.

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Amino acid

; OTHER INFORMATION: sequence coding for L chain V region of ant-TF

; OTHER INFORMATION: mouse monoclonal antibody ATR-7

US-09-647-468-163

Query Match 93.8%; Score 649; DB 4; Length 131;

Best Local Similarity 93.9%; Pred. No. 5.8e-55;

Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 MSPAQFLFLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSGKTYLNL 61

Db 1 MSPAQFLFLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSGKTYLNL 60

QY 62 LORPQSPKRLIYLVSKLDGVPDRFTGSGSGTFTLKISRIEADLGLYYCWQTHPPR 121

Db 61 LORPQSPKRLIYLVSKLDGVPDRFTGSGSGTFTLKISRIEADLGLYYCWQTHPPD 120

QY 122 TFGGKTKLEIK 132

Db 121 TFGGKTKLEIK 131

RESULT 2

US-09-647-468-164

; Sequence 164, Application US/09647468

; Patent No. 6677436

```
/ GENERAL INFORMATION:
/ APPLICANT: SATO, KOH
/ APPLICANT: ADACHI, HIDEKI
/ APPLICANT: YABUTA, NAOHITO
/ TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
/ TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
/ FILE REFERENCE: 053466/0289
/ CURRENT APPLICATION NUMBER: US/09/647,468
/ CURRENT FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: PCT/JP99/01768
/ PRIOR FILING DATE: 1999-04-02
/ PRIOR APPLICATION NUMBER: JP 10-91850
/ PRIOR FILING DATE: 1998-04-03
/ NUMBER OF SEQ ID NOS: 183
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 164
/ LENGTH: 131
/ TYPE: PRT
/ ORGANISM: Mus sp.
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Amino acid
/ OTHER INFORMATION: sequence coding for L chain V region of ant-TF
/ OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-164

Query Match      93.4%; Score 646; DB 4; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.1e-54;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY  2 MSPAQLFLVLLVWIRETNGVYVMTQPTPLSVTIGOPASISCKSSQSLDSDGKTYLNWL 61
Db  1 MSPAQLFLVLLVWIRDNGDVVLTQPTPLSVTIGOPASVCKSSQSLDSDGKTYLNWL 60
QY  62 LORPGSPKRLVLYSKLDGVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTHER 121
Db  61 LORPGSPKRLVLYSKLDGVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTHER 120
QY  122 TFGGGTKLEIK 132
Db  121 TFGGGTKLEIK 131

RESULT 3
US-09-840-459-102
/ Sequence 102, Application US/09840459
/ Patent No. 6696550
/ GENERAL INFORMATION:
/ APPLICANT: Larosa, Gregory J.
/ APPLICANT: Horvath, Christopher
/ APPLICANT: Newman, Walter
/ APPLICANT: Jones, S. Tarran
/ APPLICANT: O'Brien, Siobhan H.
/ APPLICANT: O'Keefe, Theresa
/ TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
/ TITLE OF INVENTION: METHODS OF USE THEREFOR
/ FILE REFERENCE: 1855.1052-012
/ CURRENT APPLICATION NUMBER: US/09/840,459
/ CURRENT FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: PCT/US01/03537
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 09/497,625
/ PRIOR FILING DATE: 2000-02-03
/ PRIOR APPLICATION NUMBER: 09/359,193
/ PRIOR FILING DATE: 1999-07-22
/ PRIOR APPLICATION NUMBER: 09/121,781
/ PRIOR FILING DATE: 1998-07-23
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 102
/ LENGTH: 142
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-840-459-102
```

```
/ GENERAL INFORMATION:
/ APPLICANT: SATO, KOH
/ APPLICANT: ADACHI, HIDEKI
/ APPLICANT: YABUTA, NAOHITO
/ TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
/ TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
/ FILE REFERENCE: 053466/0289
/ CURRENT APPLICATION NUMBER: US/09/647,468
/ CURRENT FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: PCT/JP99/01768
/ PRIOR FILING DATE: 1999-04-02
/ PRIOR APPLICATION NUMBER: JP 10-91850
/ PRIOR FILING DATE: 1998-04-03
/ NUMBER OF SEQ ID NOS: 183
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 164
/ LENGTH: 131
/ TYPE: PRT
/ ORGANISM: Mus sp.
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Amino acid
/ OTHER INFORMATION: sequence coding for L chain V region of ant-TF
/ OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-164

Query Match      87.6%; Score 606; DB 4; Length 142;
Best Local Similarity 93.5%; Pred. No. 8.4e-51;
Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY  10 LVLVWIRETNGVYVMTQPTPLSVTIGOPASISCKSSQSLDSDGKTYLNWLLQRPQSP 69
Db  7 LVLVWIRETNGVYVMTQPTPLSVTIGOPASISCKSSQSLDSDGKTYLNWLLQRPQSP 66
QY  70 KRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTHERFTFGGTKL 129
Db  67 KRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTHERFTFGGTKL 126
QY  130 EIK 132
Db  127 EIK 129

RESULT 4
US-09-497-625A-102
/ Sequence 102, Application US/09497625A
/ Patent No. 6727349
/ GENERAL INFORMATION:
/ APPLICANT: Larosa, Gregory J.
/ APPLICANT: Horvath, Christopher
/ APPLICANT: Newman, Walter
/ APPLICANT: Jones, S. Tarran
/ APPLICANT: O'Brien, Siobhan H.
/ APPLICANT: O'Keefe, Theresa
/ TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
/ TITLE OF INVENTION: METHODS OF USE THEREFOR
/ FILE REFERENCE: 1855.1052-004
/ CURRENT APPLICATION NUMBER: US/09/497,625A
/ CURRENT FILING DATE: 2000-02-03
/ PRIOR APPLICATION NUMBER: 09/359,193
/ PRIOR FILING DATE: 1999-07-22
/ PRIOR APPLICATION NUMBER: 09/121,781
/ PRIOR FILING DATE: 1998-07-23
/ NUMBER OF SEQ ID NOS: 106
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 102
/ LENGTH: 142
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-497-625A-102

Query Match      87.6%; Score 606; DB 4; Length 142;
Best Local Similarity 93.5%; Pred. No. 8.4e-51;
Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY  10 LVLVWIRETNGVYVMTQPTPLSVTIGOPASISCKSSQSLDSDGKTYLNWLLQRPQSP 69
Db  7 LVLVWIRETNGVYVMTQPTPLSVTIGOPASISCKSSQSLDSDGKTYLNWLLQRPQSP 66
QY  70 KRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTHERFTFGGTKL 129
Db  67 KRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTHERFTFGGTKL 126
QY  130 EIK 132
Db  127 EIK 129

RESULT 5
US-09-698-705-7
/ Sequence 7, Application US/09698705
/ Patent No. 6824780
/ GENERAL INFORMATION:
/ APPLICANT: Devaux, B.
/ APPLICANT: Keller, G.
/ APPLICANT: Koeppe, H.
/ APPLICANT: Lasky, L.
/ TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
```

```
; FILE REFERENCE: P177R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-698-705-7

Query Match      82.5%; Score 571; DB 4; Length 113;
Best Local Similarity 97.3%; Pred. No. 1.5e-47;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTTPRTFGGKLEIK 132
Db 62 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTTPRTFGGKLEIK 112

RESULT 6
US-09-698-705-12
; Sequence 12, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P177R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-12

Query Match      82.5%; Score 571; DB 4; Length 218;
Best Local Similarity 97.3%; Pred. No. 3.2e-47;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTTPRTFGGKLEIK 132
Db 62 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTTPRTFGGKLEIK 112

RESULT 7
US-09-203-958A-4
; Sequence 4, Application US/09203958A
; Patent No. 6682928
; GENERAL INFORMATION:
; APPLICANT: KELLER, Tibor
; APPLICANT: GOLDSTEIN, Joel
```

```
; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
; FILE REFERENCE: MXI-099CPA
; CURRENT APPLICATION NUMBER: US/09/203,958A
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/067232
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-203-958A-4

Query Match      81.2%; Score 562; DB 4; Length 353;
Best Local Similarity 94.6%; Pred. No. 4e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 177 VVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 236

Qy 82 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTTPRTFGGKLEIK 132
Db 237 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTTPRTFGGKLEIK 287

RESULT 8
US-09-809-739-11
; Sequence 11, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855-1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
; NAME/KEY: SITE
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (55)...(61)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (94)...(102)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-11

Query Match      80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.7e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
```

```
Db 2 VVMTQPLTSLVTVGHPASISCKSSQSLDSDGKTFLNWLLQRPQSPKRLIYLVSKLDS 61
QY 82 GVPDRFTGSGSGDFTLTKISRIEADLGLYYCWQGTFFPRTGGGKLEIK 132
Db 62 GVPDRFTGSGSGDFTLTKISRIEADLGLYYCWQGTFFPRTGGGKLEIK 112
```

```
RESULT 9
US-09-840-459-9
; Sequence 9, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-9
```

```
Query Match 80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.7e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 22 VVMTQPLTSLVTVGHPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQPLTSLVTVGHPASISCKSSQSLDSDGKTFLNWLLQRPQSPKRLIYLVSKLDS 61

QY 82 GVPDRFTGSGSGDFTLTKISRIEADLGLYYCWQGTFFPRTGGGKLEIK 132
Db 62 GVPDRFTGSGSGDFTLTKISRIEADLGLYYCWQGTFFPRTGGGKLEIK 112
```

```
RESULT 10
US-09-497-625A-9
; Sequence 9, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
```

```
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-9
```

```
Query Match 80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.7e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 22 VVMTQPLTSLVTVGHPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQPLTSLVTVGHPASISCKSSQSLDSDGKTFLNWLLQRPQSPKRLIYLVSKLDS 61

QY 82 GVPDRFTGSGSGDFTLTKISRIEADLGLYYCWQGTFFPRTGGGKLEIK 132
Db 62 GVPDRFTGSGSGDFTLTKISRIEADLGLYYCWQGTFFPRTGGGKLEIK 112
```

```
RESULT 11
US-09-419-788-113
; Sequence 113, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicity Mediated Plant Disease
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-113
```

```
Query Match 80.9%; Score 560; DB 4; Length 257;
Best Local Similarity 94.6%; Pred. No. 4.3e-46;
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 22 VVMTQPLTSLVTVGHPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 138 VLMTQAPLTVTVGHPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 197

QY 82 GVPDRFTGSGSGDFTLTKISRIEADLGLYYCWQGTFFPRTGGGKLEIK 132
Db 198 GVPDRFTGSGSGDFTLTKISRIEADLGLYYCWQGTFFPRTGGGKLEIK 248
```

```
RESULT 12
US-09-647-468-149
; Sequence 149, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
```

APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 149
LENGTH: 112
TYPE: PRT
ORGANISM: Mus sp.
FEATURES:
OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
OTHER INFORMATION: monoclonal antibody ATR-7
US-09-647-468-149

Query Match 80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 2.1e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQPTLTSVTIQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VLVTTPTLTSVTIQPASVSCSKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGGTDFTLKISRVEADLGLYYCWQGTFFPRTFGGKLEIK 132
Db 62 GVPDRFTGSGGTDFTLKISRVEADLGLYYCWQGTFFPRTFGGKLEIK 112

RESULT 13
US-09-647-468-150
Sequence 150, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 150
LENGTH: 112
TYPE: PRT
ORGANISM: Mus sp.
FEATURES:
OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
OTHER INFORMATION: monoclonal antibody ATR-8
US-09-647-468-150

Query Match 80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 2.1e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQPTLTSVTIQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VLVTTPTLTSVTIQPASVSCSKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGGTDFTLKISRVEADLGLYYCWQGTFFPRTFGGKLEIK 132
Db 62 GVPDRFTGSGGTDFTLKISRVEADLGLYYCWQGTFFPRTFGGKLEIK 112

Db 62 GVPDRFTGSGGTDFTLKISRVEADLGLYYCWQGTFFPRTFGGKLEIK 112

RESULT 14
US-09-840-459-54
Sequence 54, Application US/09840459
Patent No. 6696550
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 54
LENGTH: 112
TYPE: PRT
ORGANISM: Homo sapiens
US-09-840-459-54

Query Match 80.3%; Score 556; DB 4; Length 112;
Best Local Similarity 92.8%; Pred. No. 4e-46;
Matches 103; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTQPTLTSVTIQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 IQLTQSPILTSVTIQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGGTDFTLKISRVEADLGLYYCWQGTFFPRTFGGKLEIK 132
Db 62 GVPDRFTGSGGTDFTLKISRVEADLGLYYCWQGTFFPRTFGGKLEIK 112

RESULT 15
US-09-497-625A-54
Sequence 54, Application US/09497625A
Patent No. 6727349
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-004
CURRENT APPLICATION NUMBER: US/09/497,625A
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 54
LENGTH: 112

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-54

Query Match      80.3%; Score 556; DB 4; Length 112;
Best Local Similarity 92.8%; Pred. No. 4e-46;
Matches 103; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTOTPLTSLVTIGOPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLYSKLDS 81
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 IQLTQSPLTSLVTIGOPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLYSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEADLGYVCWQGTTHFPPTFGGTTKLEIK 132
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 GVPDRFTGSGSGTDFTLKISRVEADLGYVCWQGTTHFPPTFGGTTKLEIK 112
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Search completed: September 26, 2005, 07:19:02
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 26, 2005, 07:14:55 ; Search time 521 Seconds
(without alignments)
103.124 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLVLVIRETNG.....CWQTHPRTFGGTKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 1826554

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	692	100.0	132	14	US-10-010-942B-2
2	692	100.0	132	15	US-10-388-389-2
3	692	100.0	132	16	US-10-703-713-2
4	692	100.0	132	17	US-10-704-070-2
5	692	100.0	132	17	US-10-232-030-2
6	650	93.9	135	9	US-09-881-823-10
7	649	93.8	131	15	US-10-462-062-163
8	646	93.4	131	15	US-10-462-062-164
9	644	93.1	239	17	US-10-476-265-19
10	641	92.6	133	18	US-10-810-881A-49
11	640	92.5	132	14	US-10-010-942B-5
Sequence 2, Appli					
Sequence 2, Appli					
Sequence 2, Appli					
Sequence 2, Appli					
Sequence 10, Appl					
Sequence 163, App					
Sequence 164, App					
Sequence 19, Appl					
Sequence 49, Appl					
Sequence 5, Appli					

12	640	92.5	132	15	US-10-388-389-5	Sequence 5, Appli
13	640	92.5	132	16	US-10-703-713-5	Sequence 5, Appli
14	640	92.5	132	16	US-10-704-070-5	Sequence 5, Appli
15	640	92.5	132	17	US-10-232-030-5	Sequence 5, Appli
16	636	91.9	132	13	US-10-006-773-11	Sequence 11, Appl
17	630	91.0	132	14	US-10-010-942B-11	Sequence 11, Appl
18	630	91.0	132	15	US-10-388-389-11	Sequence 11, Appl
19	630	91.0	132	16	US-10-703-713-11	Sequence 11, Appl
20	630	91.0	132	16	US-10-704-070-11	Sequence 11, Appl
21	630	91.0	132	17	US-10-232-030-11	Sequence 11, Appl
22	618	89.3	145	16	US-10-830-899-58	Sequence 58, Appl
23	618	89.3	145	16	US-10-830-899-61	Sequence 61, Appl
24	618	89.3	145	16	US-10-830-899-61	Sequence 61, Appl
25	618	89.3	145	17	US-10-861-662-52	Sequence 52, Appl
26	618	89.3	145	17	US-10-861-662-58	Sequence 58, Appl
27	618	89.3	145	17	US-10-861-662-61	Sequence 61, Appl
28	606	87.6	142	9	US-09-840-459-102	Sequence 102, App
29	606	87.6	142	16	US-10-766-773-102	Sequence 102, App
30	606	87.6	142	16	US-10-766-610-102	Sequence 102, App
31	606	87.6	142	16	US-10-733-563-102	Sequence 102, App
32	571	82.5	113	17	US-10-937-046-7	Sequence 7, Appli
33	571	82.5	218	17	US-10-937-046-12	Sequence 12, Appli
34	562	81.2	353	10	US-09-203-958A-4	Sequence 4, Appli
35	562	81.2	353	18	US-10-764-131-4	Sequence 4, Appli
36	560	80.9	112	9	US-09-835-087-1	Sequence 1, Appli
37	560	80.9	112	9	US-09-809-739-11	Sequence 11, Appli
38	560	80.9	112	9	US-09-840-459-9	Sequence 9, Appli
39	560	80.9	112	16	US-10-766-773-9	Sequence 9, Appli
40	560	80.9	112	16	US-10-766-610-9	Sequence 9, Appli
41	560	80.9	112	16	US-10-733-563-9	Sequence 9, Appli
42	560	80.9	112	17	US-10-855-013-12	Sequence 12, Appl
43	560	80.9	122	15	US-10-272-899A-86	Sequence 86, Appl
44	560	80.9	130	15	US-10-272-899A-88	Sequence 88, Appl
45	559	80.8	112	15	US-10-462-062-149	Sequence 149, App

ALIGNMENTS

RESULT 1
US-10-010-942B-2
; Sequence 2, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: BETA AMYLOID PEPTIDE
; CURRENT APPLICATION NUMBER: US/10/010,942B
; PRIOR FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-010-942B-2

Query Match 100.0%; Score 692; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMSPAQFLFLVLVIRETNGVVMTQPLTUSVITIGQPASISCKSSQSLSDGKTYLW 60
Db 1 MMSPAQFLFLVLVIRETNGVVMTQPLTUSVITIGQPASISCKSSQSLSDGKTYLW 60

[illegible]

RESULT 2

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US-10-388-389-2
; Sequence 2, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: B2A-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388.389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-388-389-2

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	Query Match	100.0%;	Score 692;	DB 15;	Length 132;
	Best Local Similarity	100.0%;	Pred. No. 6.4e-57;		
	Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MMGPAQFLFLVLWIRETNQGVVMTQPTLTLSVTIGQPASTICKSSOSLLDSGKTYLNW	60		
Db	1	MMGPAQFLFLVLWIRETNQGVVMTQPTLTLSVTIGQPASTICKSSOSLLDSGKTYLNW	60		
Qy	61	LLQRPGSQKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIAEADGLYLYCWQGTFF	120		
Db	61	LLQRPGSQKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIAEADGLYLYCWQGTFF	120		
Qy	121	RTFGGGTKLEIK	132		
Db	121	RTFGGGTKLEIK	132		

RESULT 3

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US-10-703-713-2
; Sequence 2, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/107388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06

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; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1) ... (20)
US-10-703-713-2

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	Query Match	100.0%;	Score 692;	DB 16;	Length 132;
	Best Local Similarity	100.0%;	Pred. No. 6.4e-57;		
	Matches 132; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MMSPAQFLFLLWIRETNGYVVMOTPTLTSVTIGOPASICKSSOSILDSGKTYLNW	60		
Dd	1	MMSPAQFLFLLWIRETNGYVVMOTPTLTSVTIGOPASICKSSOSILDSGKTYLNW	60		
Qy	61	LLORPQSQPKRLIYLVSKLDSGVDPDRFTSGSGSDFTLKISRIEAEDGLGYCWMQGTHFP	120		
Dd	61	LLORPQSQPKRLIYLVSKLDSGVDPDRFTSGSGSDFTLKISRIEAEDGLGYCWMQGTHFP	120		
Qy	121	RTFGGGTKEIK	132		
Dd	121	RTFGGGTKEIK	132		

RESULT 4

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US-10-704-070-2
; Sequence 2, Application US/10704070
; Publication NO. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-704-070-2

```

Query Match	100.0%;	Score 692;	DB 16;	Length 132;
Best Local Similarity	100.0%;	Pred. No. 6.4e-57;		
Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MMSPAQFLFLVLWIRETNGYVVMTPQLTSLVTIGQPASISCKSSOSLLDSDGKTYLW	60	
Db	1	MMSPAQFLFLVLWIRETNGYVVMTPQLTSLVTIGQPASISCKSSOSLLDSDGKTYLW	60	
Qy	61	LLRPGQSPKRLIYLVSKLDGVPDRFTGSGSGDTFLTKISRFAEADGLGYCQGTHFP	120	
Db	61	LLRPGQSPKRLIYLVSKLDGVPDRFTGSGSGDTFLTKISRFAEADGLGYCQGTHFP	120	
Qy	121	RTFGGGTKLEIK	132	
Db	121	RTFGGGTKLEIK	132	

RESULT 5
US-10-232-030-2
; Sequence 2, Application US/10232030
; Publication No. US20050009150A1
; GENERAL INFORMATION:
; APPLICANT: Dale Schenk
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CN
; CURRENT APPLICATION NUMBER: US/10/232,030
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 09/723,713
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-232-030-2

Query Match 100.0%; Score 692; DB 17; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.4e-57; Mismatches 0; Indels 0; Gaps 0;
Matches 132; Conservative 0;
QY 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLW 60
DB 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLW 60
QY 61 LLQPGQSPKRLIYLVSKLDSGVPDRFTGSGSGDTFTLKISRIEADLGLYYCQGTTHP 120
DB 61 LLQPGQSPKRLIYLVSKLDSGVPDRFTGSGSGDTFTLKISRIEADLGLYYCQGTTHP 120
QY 121 RTFGGKLEIK 132
DB 121 RTFGGKLEIK 132

RESULT 6
US-09-881-823-10
; Sequence 10, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 135
; TYPE: PRT

; ORGANISM: Murine
US-09-881-823-10
Query Match 93.9%; Score 650; DB 9; Length 135;
Best Local Similarity 93.2%; Pred. No. 5.6e-53;
Matches 123; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLW 60
DB 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLW 60
QY 61 LLQPGQSPKRLIYLVSKLDSGVPDRFTGSGSGDTFTLKISRIEADLGLYYCQGTTHP 120
DB 61 LLQPGQSPKRLIYLVSKLDSGVPDRFTGSGSGDTFTLKISRIEADLGLYYCQGTTHP 120
QY 121 RTFGGKLEIK 132
DB 121 RTFGGKLEIK 132

RESULT 7
US-10-462-062-163
; Sequence 163, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053465-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for L chain V region of anti-Tf mouse monoclonal
; OTHER INFORMATION: antibody ATR-7
US-10-462-062-163

Query Match 93.8%; Score 649; DB 15; Length 131;
Best Local Similarity 93.9%; Pred. No. 6.7e-53;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLW 61
DB 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLW 60
QY 62 LLQPGQSPKRLIYLVSKLDSGVPDRFTGSGSGDTFTLKISRIEADLGLYYCQGTTHP 121
DB 61 LLQPGQSPKRLIYLVSKLDSGVPDRFTGSGSGDTFTLKISRIEADLGLYYCQGTTHP 120
QY 122 RTFGGKLEIK 132
DB 121 RTFGGKLEIK 131

RESULT 8
US-10-462-062-164
; Sequence 164, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

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/ TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
/ FILE REFERENCE: 053466-0360
/ CURRENT APPLICATION NUMBER: US/10/462,062
/ CURRENT FILING DATE: 2003-06-16
/ PRIOR APPLICATION NUMBER: PCT/JP99/01768
/ PRIOR FILING DATE: 1999-04-02
/ PRIOR APPLICATION NUMBER: JP 10-91850
/ PRIOR FILING DATE: 1998-04-03
/ NUMBER OF SEQ ID NOS: 183
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 164
/ LENGTH: 131
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
/ OTHER INFORMATION: sequence for L chain V region of anti-TP mouse monoclonal
/ OTHER INFORMATION: antibody ATTR-8
US-10-462-062-164

Query Match          93.4%; Score 646; DB 15; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.3e-52;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 MSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNL 61
DB 1 MSPAQFLFLVLWIRDINGDVLTQTPLTSLVTIGQPASVCKSSQSLDSDGKTYLNL 60

QY 62 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTFLKISRVEADLGLYYCWOQTHPPR 121
DB 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTFLKISRVEADLGLYYCWOQTHPPD 120

QY 122 TFGGGTKLEIK 132
DB 121 TFGGGTKLEIK 131

RESULT 9
US-10-476-265-19
/ Sequence 19, Application US/10476265
/ Publication No. US20050090648A1
/ GENERAL INFORMATION:
/ APPLICANT: Eli Lilly and Company
/ TITLE OF INVENTION: Humanized Antibodies
/ FILE REFERENCE: X14958
/ CURRENT APPLICATION NUMBER: US/10/476,265
/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: 60/287539
/ PRIOR FILING DATE: 2001-04-30
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 19
/ LENGTH: 239
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: humanized antibody
US-10-476-265-19

Query Match          93.1%; Score 644; DB 17; Length 239;
Best Local Similarity 90.9%; Pred. No. 3.9e-52;
Matches 120; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNL 60
DB 1 MMSPAQFLFLVLWIRETNGYVVMVTQSPLSPLVTIGQPASISCKSSQSLDSDGKTYLNL 60

QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTFLKISRVEADLGLYYCWOQTHPP 120
DB 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTFLKISRVEADLGLYYCWOQTHPP 120

QY 121 RTFGGGTKLEIK 132
DB 121 RTFGGGTKLEIK 132
```

```
DB 121 RTFGGGTKVEIK 132

RESULT 10
US-10-810-881A-49
/ Sequence 49, Application US/10810881A
/ Publication No. US20050129695A1
/ GENERAL INFORMATION:
/ APPLICANT: MerckKen, Marc; Benson, Jacqueline M.
/ TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
/ FILE REFERENCE: CEN5021 NP
/ CURRENT APPLICATION NUMBER: US/10/810,881A
/ CURRENT FILING DATE: 2004-03-26
/ PRIOR APPLICATION NUMBER: US 60/458,474
/ PRIOR FILING DATE: 2003-03-28
/ PRIOR APPLICATION NUMBER: US 60/458,469
/ PRIOR FILING DATE: 2003-03-28
/ PRIOR APPLICATION NUMBER: US 60/458,509
/ PRIOR FILING DATE: 2003-03-28
/ PRIOR APPLICATION NUMBER: US 60/458,510
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 49
/ LENGTH: 133
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)..(20)
/ OTHER INFORMATION: Signal Peptide
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (21)..(43)
/ OTHER INFORMATION: FR1
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (44)..(59)
/ OTHER INFORMATION: CDR1
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (60)..(74)
/ OTHER INFORMATION: FR2
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (75)..(81)
/ OTHER INFORMATION: CDR2
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (82)..(113)
/ OTHER INFORMATION: FR3
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (114)..(122)
/ OTHER INFORMATION: CDR3
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (123)..(133)
/ OTHER INFORMATION: FR4/J region
US-10-810-881A-49

Query Match          92.6%; Score 641; DB 18; Length 133;
Best Local Similarity 91.7%; Pred. No. 3.8e-52;
Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNL 60
DB 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLSW 60

QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTFLKISRVEADLGLYYCWOQTHPP 120
DB 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTFLKISRVEADLGLYYCWOQTHPP 120
```

```

Qy 121 RTFGGTYKLEIK 132
    ||||| ||||
Db 121 RTFGGTYKLEIK 132

RESULT 11
US-10-010-942B-5
; Sequence 5, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
; US-10-010-942B-5

Query Match 92.5%; Score 640; DB 14; Length 132;
Best Local Similarity 90.2%; Pred. No. 4,7e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0

Qy 1 MMSPAQFLFLVLVIRETNGVVMQTPLTSLVTIGQPASISCKSSQSLLSDGKTYLNW 60
Db 1 MMSPAQFLFLVLVIRETNGVVMQTQSPLSLPVTPGEPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVAEDLGLYYCWQGTFFP 120
Db 61 LLQPGQSPQRLIYLVSKLDSGVDPDRFSGSGGTDFTLKISRVAEDVGVYYCWQGTFFP 120

Qy 121 RTFGGTYKLEIK 132
    ||||| ||||
Db 121 RTFGGTYKLEIK 132

RESULT 12
US-10-388-389-5
; Sequence 5, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

```

; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurik
; APPLICANT: Saldanha, Jose
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/704,070
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-704-070-5
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```

Query Match          92.5%; Score 640; DB 16; Length 132;
Best Local Similarity 90.2%; Pred. No. 4.7e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY      1  MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNN 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1  MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNN 60

QY      61  LIQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTTHP 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61  LIQKPGSQPRLIYLVSKLDSGVDPDRFSGSGSGTDFTLKISRVEADVGVYYCWQGTTHP 120

QY      121  RTFGGQTKLEIK 132
      |||:|||||:|||||
Db      121  RTFGQGTKEIK 132
```

```

RESULT 15
US-10-232-030-5
; Sequence 5, Application US/10232030
; Publication No. US2005009150A1
; GENERAL INFORMATION:
; APPLICANT: Dale Schenk
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CN
; CURRENT APPLICATION NUMBER: US/10/232,030
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 09/723,713
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-232-030-5

Query Match          92.5%; Score 640; DB 17; Length 132;
Best Local Similarity 90.2%; Pred. No. 4.7e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY      1  MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNN 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1  MMSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNN 60

QY      61  LIQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTTHP 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61  LIQKPGSQPRLIYLVSKLDSGVDPDRFSGSGSGTDFTLKISRVEADVGVYYCWQGTTHP 120

QY      121  RTFGGQTKLEIK 132
      |||:|||||:|||||
Db      121  RTFGQGTKEIK 132
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Search completed: September 26, 2005, 07:27:49
Job time : 521 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 04:38:08 ; Search time 2359 Seconds
(without alignments)
6389.763 Million cell updates/sec

Title: US-10-010-942B-1
Perfect score: 396
Sequence: 1 atgatgagtcctgccagtt.....gcaccaagctggaatcaaa 396

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	368.8	93.1	773	4	BG964451 602832101
2	357.6	90.3	909	4	BI105366 602893669
3	312.4	78.9	926	2	BF301241 602029676
4	311.2	78.6	783	6	CB316492 AGENCOURT
5	310.8	78.5	407	5	BY223114 BY223114
6	307.8	77.7	357	5	BY344116 BY344116
7	306	77.3	618	8	AZ938720 2M0197H20
8	300.4	75.9	356	5	BY216837 BY216837
9	297.8	75.2	883	2	BF134462 601784859
10	290.4	73.3	346	5	BY216432 BY216432
11	290.4	73.3	346	5	BY219888 BY219888
12	288.2	72.8	355	5	BY217354 BY217354
13	274.4	69.3	342	5	BY215445 BY215445
14	266	67.2	312	5	BY346516 BY346516
15	263.2	66.5	960	5	BO711007 AGENCOURT
16	260.8	65.9	833	7	CO565696 AGENCOURT
17	260.6	65.8	898	5	BQ708918 AGENCOURT
18	260	65.7	525	6	CD696039 EST12562
19	258.4	65.3	634	4	BM783161 K-EST0061
20	257.6	65.1	952	4	BG758592 602712820
21	256.8	64.8	681	5	BU930837 AGENCOURT
22	256.8	64.8	816	4	BI759427 603043095
23	255.8	64.6	614	2	AW405187 UI-HF-BL0
24	255.2	64.4	475	6	CD699289 EST15812

ALIGNMENTS

RESULT 1
LOCUS BG964451 773 bp mRNA linear EST 12-JUN-2001
DEFINITION 602832101F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4986529 5',
mRNA sequence.
ACCESSION BG964451
VERSION BG964451.1 GI:14352088
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 773)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM10996 row: b column: 02
High quality sequence stop: 732.
Location/Qualifiers
1. 773
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 93.1%; Score 368.8; DB 4; Length 773;
Best Local Similarity 95.7%; Pred. No. 1.9e-105;
Matches 379; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Oy 1 ATGATGAGTCTGCGCCAGTTCCTCTTTCTGTGTAGTCTCGGATTCGGAAACCAACCGT 60

Query Match 78.9%; Score 312.4; DB 2; Length 926;
Best Local Similarity 96.7%; Pred. No. 1.6e-87;
Matches 383; Conservative 0; Mismatches 6; Indels 7; Gaps 6;
QY 1 ATGATGAGTCTGCCAGTCTCTGTTCTGTTAGTGTCTGATTCGGGAACCAACGGT 60
DB 43 ATGATGAGTCTGCCAGTCTCTGTTCTGTTAGTGTCTGATTCGGGAACCAACGGT 102
QY 61 TATGTTGTGATGACCCAGACCTCCACTCACTTTGTCGGTTACCATTTGGACAACCAACGCTCC 120
DB 103 GATG-TGTGATGACCCAGACCTCCACTCAC-TGTGCGGTTACCA-TGGACAACCAACGCTCC 159
QY 121 ATCTCTTCCAAAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGAAAGACATATTGGAATTGG 180
DB 160 ATCTCTTCCAAAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGAAAGACATATTGGAAT--G 217
QY 181 TTGTTTACAGAGCCAGGCGAGTCTCCAAAGCGCTTAATCTATCTGTTGCTCTAAACTGGAC 240
DB 218 GTGTTTACAGAGCCAGGCGAGTCTCCAAAGCGCTTAATCTATCTGTTGCTCTAAACTGGAC 277
QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 300
DB 278 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 337
QY 301 AGCAGAATAGAGGCTGAGAGTTTGGAGCTTTTATTATTCTGCTGGCAAGGTACACATTTTCCT 360
DB 338 AGCAGAGTGGAGGCTGAGGA-TTGGAGTTTTATTATTCTGCTGGCAAGGTACACATTTTCCT 396
QY 361 CGGAGTTCGGTGGAGGCGACCAAGCTGGAATCAAA 396
DB 397 -GGACGTTTCGGTGGAGGCGACCAAGCTGGAATCAAA 431
RESULT 4
LOCUS CB316492 783 bp mRNA linear EST 04-MAR-2003
DEFINITION AGNCOURT_11790259 NICHD_Rr_Pit1 Rattus norvegicus cDNA clone
IMAGE:6890409 5', mRNA sequence.
ACCESSION CB316492
VERSION CB316492.1 GI:28840727
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 783)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: John C. Marshall, M.D., Ph.D
cDNA Library Preparation: CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM3149 row: n column: 08
High quality sequence stop: 568.
Location/Qualifiers
1. 783
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:6890409"
/tissue_type="Pituitary"
/lab_host="DH10B"
/clone_lib="NICHD_Rr_Pit1"
/note="vector: pONR-LiB; Site_1: SfiI; Site_2: SfiI; 5'

and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCATG-dt(30)BN-3' (where B = A, C, G, or T). Average insert size 1.23 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN
Query Match 78.6%; Score 311.2; DB 6; Length 783;
Best Local Similarity 86.6%; Pred. No. 3.6e-87;
Matches 343; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1 ATGATGAGTCTGCCAGTTCCTCTTTCTGTTAGTGTCTCGATTCGGGAACCAACGGT 60
DB 36 ATGATGAGTCTGCCAGTTCCTCTTTCTGCTAATGCTCTGGATCCAGGAAGCCGCGGA 95
QY 61 TATGTTGTGATGACCCAGACCTCCACTCACTTTGTCGGTTACCATTTGGACAACCAACGCTCC 120
DB 96 GATGTTGTGATGACCCAGACCTCCACTCTTTTGTGGTTGCCATTTGGACAATCACTGCTCC 155
QY 121 ATCTCTTTCGAAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGAAAGACATATTTGAATTGG 180
DB 156 ATCTCTTTCGAAGTCAAGTCAGAGCCTCTGATATAGTATGGAAGACATATTTGCATTGG 215
QY 181 TTGTTTACAGAGGCGAGGCGAGTCTCCAAAGCGCTTAATCTATCTGTTGCTCTAAACTGGAC 240
DB 216 TTATTTACAGAGTCTCGGAGGCTCTCCGAAGCGCTTAATCTATCAGGTGCTCTAACTGGGC 275
QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 300
DB 276 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGAAGAAGATTTTACACTTAAATC 335
QY 301 AGCAGAATAGAGGCTGAGGATTTTGGGACTTTTATTATTGCTGCGCAAGGTACACATTTTCCT 360
DB 336 AGCAGAGTGGAGGCTGGAAGTTTGGAGTTTATTCTGCGCGCAACTATACATTTTCG 395
QY 361 CGGAGTTCGGTGGAGGCGACCAAGCTGGAATCAAA 396
DB 396 CTCAGTTTCGGTCTCGGAGCCCAAGCTGGAGATCAAA 431
RESULT 5
LOCUS BY223114 407 bp mRNA linear EST 10-DEC-2002
DEFINITION BY223114 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830301N12 5', mRNA sequence.
ACCESSION BY223114
VERSION BY223114.1 GI:26404217
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 407)
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, K., I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matesuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gutencich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawabawa, Y., Kedzierski, R.M., King, B.L., Kongaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

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Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome-gsc.riken.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

RESULT 6 BY344116 LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Query Match

Best Local Similarity

Matches 350; Conservative

0; Mismatches

27; Indels

3; Gaps

2;

QY

Db

QY

Db

121 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGAAAGACATATTTGAATTGG 180

151 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGAAAGACATATTTGAATTGG 210

181 TTGTTACAGAGCCAGGCGAGTCTTCAAGGCCCTTAATCTATCTGCTGTCTAAACTGGAC 240

211 TTATTTACAGAGCCAGGCGAGTCTTCAAGGCCCTTAATCTATCTGCTGTCTAAACTGGAA 270

241 TCTGAGTCCCTTGACAGGTTTCACTGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 300

271 TCTGAGTCCCTTGACAGGTTTCACTGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 328

301 AGCAGATAGAGGCTGAGGATTTGGGACCTTTATTATTGCTGCTCAAGGTTACACATTTTCT 360

329 ACCAGAGTGTGAGGCTGAGGATTTGGGA-GTATTACTGCTGCAAGCTACACATTTTCT 387

361 CGGACGTTGCTGAGGAGGCAC 380

388 CAGACGTTTGGTGGAGGCAC 407

BY344116 357 bp mRNA linear EST 12-DEC-2002

clone L730002K22 5', mRNA sequence.

BY344116 GI:26573604

EST.

Mus musculus (house mouse)

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 357)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Oساتو, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothe, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Negashima, I., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

FEATURES source

Location/Qualifiers

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/organism="Mus musculus"

/mol_type="mRNA"

/strain="NOD"

/db_xref="taxon:10090"

/clone="F83030N12"

/tissue_type="activated spleen"

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Best Local Similarity 92.1%; Pred. No. 4.1e-87;

Matches 350; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

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Db 91 GATGTTGTGATGATCCAGATCCACTCCTTGTGCGGTACCATTTGGACCAACGAGCTCC 150

Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hiroyane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Vassilis Aidinis (Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece) whose assistance we gratefully
acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES source
Location/Qualifiers
1..357
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L730002K22"
/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"

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Query Match 77.7%; Score 307.8; DB 5; Length 357;
Best Local Similarity 96.3%; Pred. No. 3.5e-86;
Matches 315; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ATGATGAGTCTGCCAGTCTCTGTTCTGTTAGTCTCTGATTCGGGAACCAACCGGT 60
Db |||||
31 ATGATGAGTCTGCCAGTCTCTGTTCTGTTAGTCTCTGATTCGGGAACCAACCGGT 90
Qy |||||
Db |||||
61 TATGTTGTGATGACCCAGTCTCACTTCTGCGTTACCATTTGGACACAGCCCTCC 120
Qy |||||
Db |||||
91 GATGTTGTGATGACCCAGTCTCACTTCTGCGTTACCATTTGGACACAGCCCTCT 150
Qy |||||
Db |||||
121 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGATAGTATGATGAACATATTTGAATTGG 180
Qy |||||
Db |||||
151 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGATAGTATGATGAACATATTTGAATTGG 210
Qy |||||
Db |||||
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Qy |||||
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Qy |||||
Db |||||
301 AGCAGATAGAGGCTGAGGATTTGGGA 327
Qy |||||
Db |||||
331 AGCAGATAGAGGCTGAGGATTTGGGA 357

RESULT 7
AZ938720 618 bp DNA linear GSS 26-APR-2001
LOCUS 2M0197H20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION

clone UUGC2M0197H20 F, genomic survey sequence.
AZ938720 1 GI:13798758
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 618)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0197 row: H column: 20
Seq primer: CGTTGTAAACGACGCCGCGT
Class: plasmid ends
High quality sequence stop: 618.
Location/Qualifiers
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/sex="Female"
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 77.3%; Score 306; DB 8; Length 618;
Best Local Similarity 96.6%; Pred. No. 1.5e-85;
Matches 312; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 43 ATTCGGGAACCAACGGTATGTTGTATGATGCCAGACTCCACTCACCTTTGCGGTTACC 102
Db |||||
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103 ATTGGACAACCAACGGCTCCATCTCTTGAAGTCAAGTCAGAGCCTCTTAGATAGTATGGA 162
Qy |||||
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288 ATTGGACAACCAACGGCTCCATCTCTTGAAGTCAAGTCAGAGCCTCTTAGATAGTATGGA 347
Qy |||||
163 AAGACATATTTGAATGTTGTTTACAGAGGCCAGCCAGTCTCCAAAGCGCTTAATCTAT 222

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Qy 223 CTGGTGTCTAAACTGACCTCTGGAGTCCCTGACAGGTTCACTGGCAGTGATCAGGACA 282
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Qy 283 GATTTTACACTGAAATACAGCAGNATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGG 342
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Qy 343 CAAGGTACACTATTTTCTCTCGGAC 365
Db 528 CAAGGTACACTATTTTCTCTCACAC 550

RESULT 8
BY216837 356 bp mRNA linear EST 10-DEC-2002
LOCUS BY216837 RIKEN full-length enriched, activated spleen Mus musculus
DEFINITION CDNA clone F830047E03 5', mRNA sequence.

ACCESSION BY216837
VERSION BY216837.1 GI:26397609
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 356)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.B., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL MEDLINE
PUBMED
COMMENT Contact: Yoshihide Hayashizaki
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC Building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F830047E03"
/tissue_type="activated spleen"
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Matches 310; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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Qy 181 TTGTTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGCTGTCTAAACTGGAC 240
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Qy 241 TCTGAGTCCCTGACAGAGTTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC 300
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RESULT 9
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BF134462 mRNA sequence.
ACCESSION BF134462
VERSION BF134462.1 GI:10973502
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 883)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsbgs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9254 row: e column: 15
High quality sequence stop: 708.
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4012790"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu30"
/note="Torgan; lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
ORIGIN
Query Match 75.2%; Score 297.8; DB 2; Length 883;
Best Local Similarity 94.2%; Pred. No. 6.7e-83;
Matches 374; Conservative 0; Mismatches 17; Indels 6; Gaps 6;
QY 1 ATGATGAGTCTGCCAGTCTCTGTTCTGTAGTCTGATTCGGGAACCAACCGT 60
DB 19 ATGATGAGTCTGCCAGTCTCTGTTCTGTAGTCTGATTCGGGAACCAACCGT 78
QY 61 TATGTTGTGATGACCAAGTCCACTCTACTTGTGCGTTACCATGGCAACCAAGCTCC 120
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QY 240 CTCTGAGTCCCTGACAGGTTCACTGCGAGTGGATCAGGACAGATTTTACACTGAAAT 299
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QY 300 CAGCAATAGAGGCTGAGGATTTGGGACTTTATTTATTTGCTGGCAAGTACACATTTTCC 359
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QY 360 TCGGAGCTTGGTGGAGGCCAAGCTCGAATCAAA 396
DB 374 TCGGAGCTTGGTGGAGGCCAAGCTCGAATCAAA 410
RESULT 10
LOCUS BY216432 346 bp mRNA linear EST 10-DEC-2002.
DEFINITION BY216432 RIKEN full-length enriched, activated spleen Mus musculus
cDNA clone F83044L02 5', mRNA sequence.

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ACCESSION BY216432
VERSION BY216432.1 GI:26397182
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 346)
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusci, V.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Guertincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
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Nature 420, 563-573 (2002)
12466851
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
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Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose

```


Qy 121 ATCTCTGCAAGTCAAGTCAGAGCTCTTAGATAGTGAAGACATATTTGAATTGG 180
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RESULT 12
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 ACCESSION BY217354
 VERSION BY217354.1 GI:26398178
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (Bases 1 to 355)
 REFERENCES
 AUTHORS
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaado, I., Osato, N., Saito, R., Suzuki, H., Yanagawa, Y., Nogami, A.,
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 Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,
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 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
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 JOURNAL 22354683
 MEDLINE
 PUBMED 12466851
 COMMENT
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 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
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 Computer-based methods for the mouse full-length cDNA
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 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

Source
 1. 355
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="NOD"
 /db_xref="taxon:10090"
 /clone="F830050M02"
 /tissue type="activated spleen"
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RESULT 13
 BY215445 342 bp mRNA linear EST 10-DEC-2002
 LOCUS BY215445
 DEFINITION BY215445 RIKEN full-length enriched, activated spleen Mus musculus
 cDNA clone F830037C03 5', mRNA sequence.
 ACCESSION BY215445
 VERSION BY215445.1 GI:26396173

KEYWORDS

SOURCE

ORGANISM

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 342)

REFERENCE

AUTHORS

FEATURES

source

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/clone_lib="RIKEN full-length enriched, activated spleen"

further details.

Location/Qualifiers

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/clone_lib="RIKEN full-length enriched, activated spleen"

ORIGIN

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 Matches 295; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 1 ATGATGAGTCTGCCAGGTTCTCTGTTCTGTTAGTGCTCTGATTCGGGAACCAACCGT 60
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 Db 31 ATGATGAGTCTGCCAGGTTCTCTGTTCTGTTAGTGCTCTGATTCGGGAACCAACCGT 90
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QY 61 TATGTTGTGATGACCCAGACTCCACTCTTGTCTGCTTACCATTTGGACCAACCGCTCC 120
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 Db 331 CAGCAGATGGA 342

RESULT 14

BY346516

LOCUS

BY346516 RIKEN full-length enriched, whole joints Mus musculus cDNA

clone L730024N10 5', mRNA sequence.

BY346516.1 GI:26576004

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus (house mouse)

Mus musculus

Mus musculus

Mus musculus

Mus musculus

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Mus musculus

Mus musculus

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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 342)

Okazaki, Y., Furuno, M., Saito, R., Suzuki, H., Yamanaka, I.,

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Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

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Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

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Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics

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Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

Location/Qualifiers

1. 312

/organism="Mus musculus"

/mol_type="mRNA"

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/clone="L730024N10"

/tissue_type="whole joints"

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Matches 272; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 61 TATGTTGTGATGACCCAGACTCCACTCTTTGTGCGTTTACCATTTGGACAACCAACCGTCC 120

DB 91 GATGTTGTGATGACCCAGACTCCACTCTTTGTGCGTTTACCATTTGGACAACCAACCGTCT 150

QY 121 ATCTCTTGAAGTCAAGTCAGAGCCCTCTTAGATAGTGATGGAAGACATATTTGAATTGG 180

DB 151 ATCTCTTGAAGTCAAGTCAGAGCCCTCTTATATAGTAATGGAACCACTATTTGAATTGG 210

QY 181 TTGTTACAGAGCCAGCCAGTCTCCAAAGCCCTAATCTATCTGTGTCTTAAACTGGAC 240

DB 211 TTATTCAGAGCCAGCCAGTCTCCAAAGCCCTAATCTATCTGTGTCTTAAACTGGAC 270

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DB 271 TCTGGAGTCCCTGACAGGTTTCACATGGCAGTGGATCAGGACCA 312

RESULT 15

BQ711007

LOCUS

DEFINITION

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ711007 960 bp mRNA linear EST 16-JUL-2002

AGENCOURT 797525 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215018

BQ711007

BQ711007.1 GI:21849906

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 960)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LICM283 row: e column: 03

High quality sequence stop: 462.

FEATURES

source

1. 960

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6215018"

/lab_host="DH10B (phage-resistant)"

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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 66.5%; Score 263.2; DB 5; Length 960;

Best Local Similarity 79.0%; Pred. No. 6.5e-72;

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QY 1 ATGATGAGTCTGCCAGTCTCTGTTTCTGTAGTGCTCTGGATTCGGGAACCAACCGT 60

DB 3 ATGAGGCTCCCTGCTCAGCTCTCGGGGCTGCTAATGCTCTGGATACCTGGATCCAGTGCA 62

QY 61 TATCTGTGATGACCCAGACTCCACTCTTTGTGCGTTTACCATTGGACAACCAACCGTCC 120

DB 63 GATATTGTGATGACCCAGACTCCACTCTCTCTGTCGTCACCCCTGGACACGCGCTCC 122

QY 121 ATCTCTTGAAGTCAAGTCAGAGCCCTCTTAGATAGTGATGGAAGACATATTTGAATTGG 180

DB 123 ATCTCTGCAAGTCTAGTCAGAGCCCTCTCCATAGTAGTGAAGACACCTTTTGTATTGG 182

QY 181 TTGTTACAGAGCCAGCCAGTCTCCAAAGCCCTAATCTATCTGTGTCTTAAACTGGAC 240

Db	183	TACCTGCAGAGCCAGGCCAGCCTCCACAGCTCCTGATCTATGAGGTTTCCAAACCGGTTTC	242
Qy	241	TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC	300
Db	243	TCTGGAGTGCCAGATAGGTTTCAGTGGCAGCGGGTCAGGGACAGATTTACACTGAAATC	302
Qy	301	AGCAGATAGAGGCTGAGGATTTGGGACTTTTATTATTGCTGGCAAAGGTACACATTTTCCT	360
Db	303	AGCCGGGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGTATACAGTTTCCT	362
Qy	361	CGGACGTTGCGTGGAGGCACCAAGCTGGAAATCAAA	396
Db	363	CTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA	398

Search completed: September 26, 2005, 06:27:24
Job time : 2364 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 01:45:09 ; Search time 393 Seconds
(without alignments)
5964.930 Million cell updates/sec

Title: US-10-010-942B-1

Perfect score: 396

Sequence: 1 atgatgagctctgccagtt.....gcaccaagctggaaatcaaa 396

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	396	100.0	396	13	ADR88405
2	384	97.0	384	6	AB559426
3	370.6	93.6	717	12	ADP45590
4	368.8	93.1	420	6	ABN84610
5	365.8	92.4	717	12	ADM72032
6	364	91.9	717	8	AB224632
7	364	91.9	1953	8	AB224634
8	361	91.2	393	2	AAZ33016
9	361	91.2	393	2	AAQ23017
10	360.8	91.1	426	2	AAQ12063
11	360.8	91.1	426	2	AAQ12019
12	359.8	90.9	729	8	ABX16570
13	344.8	87.1	737	2	AAQ25691
14	335.4	84.7	426	4	AAQ13177
15	335.4	84.7	426	13	ADQ89317
16	335.4	84.7	426	13	ADQ89323
17	324.2	81.9	717	12	ADM72034
18	322.2	81.4	1135	2	AAK58936
19	317.2	80.1	976	2	AAQ25665
20	315.8	79.7	336	9	ACC84730

21	315.8	79.7	336	12	ADQ31244	Adq31244 Murine 1A
22	315.2	79.6	486	10	ADE06759	Ade06759 D13 light
23	312.8	79.0	336	2	AAV20601	Aav20601 A77 anti-
24	312.8	79.0	336	4	AAF74891	Aaf74891 A77 anti-
25	312.8	79.0	336	4	AAD15262	Aad15262 Murine A7
26	312.6	78.9	729	2	AAV36236	Aav36236 DNA of Sc
27	310	78.3	366	12	AAV35989	Adj35989 Immunoglo
28	310	78.3	390	12	ADJ95991	Adj95991 Immunoglo
29	309.8	78.2	1749	13	ADS17377	Adsl7377 Nucleotid
30	309.6	78.2	381	4	AAH21232	Aah21232 Murine de
31	307.8	77.7	768	2	AAQ48000	Aat48000 Coding se
32	306.6	77.4	315	2	AAQ20307	Aac20307 B cell by
33	306.2	77.3	336	9	ACF79290	Acf79290 Monoclonal
34	306.2	77.3	339	10	ADD05269	Adm05269 Female mo
35	306.2	77.3	339	12	ADM80360	Adm80360 Murine ho
36	306.2	77.3	749	2	AAT86234	Aat86234 Anti-huma
37	306.2	77.3	1611	2	AAT86221	Aat86221 Human p53
38	303.2	76.6	342	12	ADI26468	Adi26468 Murine I4
39	301.4	76.1	336	10	ADE13217	Adel13217 Humanised
40	301.4	76.1	339	3	ABK15814	Abk15814 DNA encod
41	301.4	76.1	339	3	AAA62120	Aaa62120 Mouse HBV
42	301	76.0	685	4	AAH77316	Aah77316 Igg Fab-B
43	298.2	75.3	819	2	AAT86646	Aat86646 Mus muscu
44	296.6	74.9	336	2	AAK58687	Aax58687 Monoclonal
45	296.6	74.9	336	5	AAI70097	Aai70097 Type II C

ALIGNMENTS

RESULT 1
ADR88405
ID ADR88405 standard; DNA; 396 BP.
XX ADR88405;
XX 16-DEC-2004 (first entry)
XX Murine 3D6 immunoglobulin light chain variable region DNA SEQ ID NO:1.
XX ds; 3D6; light chain variable region; immunoglobulin;
KW complementarity determining region; CDR; 105; variable framework region;
KW neuroprotective; nootropic; gene therapy; amyloidogenic disease;
KW Alzheimer's disease.
XX Mus musculus.
XX OS
XX Key Location/Qualifiers
XX CDS 1..396
FT /*tag= b
FT /partial
FT /note= "no stop codon given"
FT /product= "3D6 immunoglobulin light chain variable
FT region"
FT sig_peptide 1..60
FT mat_peptide 61..393
FT /*tag= c
XX WO2004080419-A2.
XX 23-SEP-2004.
XX 12-MAR-2004; 2004WO-US007503.
XX 12-MAR-2003; 2003US-00388389.
XX (NEUR-) NEURALAB LTD.
XX (AMHP) WYETH.
XX Basi G, Saldanha JW, Yednock T;
XX WPI; 2004-668880/65.
DR

DR N-PSDB; ADR88406.
XX New humanized antibodies that recognize beta amyloid peptides, useful for
PT preventing or treating amyloidogenic diseases, such as Alzheimer's
PT disease.
XX
XX Claim 76; SEQ ID NO 1; 176pp; English.
XX
XX The invention relates to a novel humanised immunoglobulin light or heavy
CC chain. The humanised immunoglobulin light or heavy chain comprises:
CC variable region complementarity determining regions (CDR's) from the 3D6
CC immunoglobulin light chain variable region sequence of 132 amino acids
CC fully defined in the specification (ADR88406), or heavy chain variable
CC region sequence of 138 amino acids fully defined in the specification
CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region
CC sequence of 131 amino acids given in the specification (ADR88418) or
CC heavy chain variable region sequence of 142 amino acids fully defined in
CC the specification (ADR88420); and a variable framework region from a
CC human acceptor immunoglobulin light or heavy chain sequence, provided
CC that at least one framework residue is substituted with the corresponding
CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
CC variable region sequence, where the framework residue is a residue that
CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
CC -interacting residue or a residue participating in the VL-VH interface.
CC An antibody of the invention has neuroprotective and neurotropic activity,
CC and may have a use in gene therapy. The composition and methods are
CC useful for preventing or treating an amyloidogenic disease, such as
CC Alzheimer's disease. The variable region sequence is useful in producing
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
CC chain, or its domain. The present sequence encodes the murine 3D6
XX immunoglobulin light chain variable region.
XX
SQ Sequence 396 BP; 101 A; 88 C; 99 G; 108 T; 0 U; 0 Other;

Query Match 100.0%; Score 396; DB 13; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.2e-119;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGAGTCTGCCAGTCTCTGTTCTCTGTTAGTCTCTGGATTCCGGAAACCAACGGT 60
DB 1 ATGATGAGTCTGCCAGTCTCTGTTCTCTGTTAGTCTCTGGATTCCGGAAACCAACGGT 60
QY 61 TATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 61 TATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 121 ATCTCTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 180
DB 121 ATCTCTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 180
QY 181 TTGTTACAGAGCCAGCCAGTCTCCAAAGCGCTTAATCTATCTGCTGCTAAACCTGGAC 240
DB 181 TTGTTACAGAGCCAGCCAGTCTCCAAAGCGCTTAATCTATCTGCTGCTAAACCTGGAC 240
QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACCTGAAATTC 300
DB 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACCTGAAATTC 300
QY 301 AGCAGAAATAGAGGCTGAGGATTTGGGACTTTATTTATGCTGGCAAGGTACACATTTTCT 360
DB 301 AGCAGAAATAGAGGCTGAGGATTTGGGACTTTATTTATGCTGGCAAGGTACACATTTTCT 360
QY 361 CGGACCTTTCGGTGGAGCCAGCAAGCTGGAATCAAA 396
DB 361 CGGACCTTTCGGTGGAGCCAGCAAGCTGGAATCAAA 396

RESULT 2
ID ABS59426
XX ID ABS59426 standard; DNA; 384 BP.
XX
AC ABS59426;
XX

DT 05-NOV-2002 (first entry)
XX Mouse 3D6 VL gene.
XX
XX Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW neurotropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta; gene; ds.
XX
OS Mus musculus.
XX
XX WO200246237-A2.
XX 13-JUN-2002.
XX
XX 06-DEC-2001; 2001WO-US046587.
XX
XX 06-DEC-2000; 2000US-0251892P.
XX
XX (NEUR-) NEURALAB LTD.
XX (AMHP) WYETH.
XX
XX Basi G, Saldanha J, Yednock T;
PI
XX
XX WPI; 2002-519658/55.
DR P-PSDB; ABC76923.
XX
XX Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
XX Claim 76; Page 79; 171pp; English.
XX
XX The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present nucleic
CC acid sequence encodes a mouse 3D6/10D5 variable light (VL) chain or
CC variable heavy (VH) chain protein of the invention
XX
SQ Sequence 384 BP; 95 A; 86 C; 97 G; 106 T; 0 U; 0 Other;
Query Match 97.0%; Score 384; DB 6; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGAGTCTGCCAGTCTCTGTTCTCTGTTAGTCTCTGGATTCCGGAAACCAACGGT 60
DB 1 ATGATGAGTCTGCCAGTCTCTGTTCTCTGTTAGTCTCTGGATTCCGGAAACCAACGGT 60
QY 61 TATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 61 TATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 121 ATCTCTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 180
DB 121 ATCTCTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 180
QY 181 TTGTTACAGAGCCAGCCAGTCTCCAAAGCGCTTAATCTATCTGCTGCTAAACCTGGAC 240
DB 181 TTGTTACAGAGCCAGCCAGTCTCCAAAGCGCTTAATCTATCTGCTGCTAAACCTGGAC 240
QY 241 TCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGACAGATTTTACCTGAAATTC 300
DB 241 TCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGACAGATTTTACCTGAAATTC 300
QY 301 AGCAGAAATAGAGGCTGAGGATTTGGGACTTTATTTATGCTGGCAAGGTACACATTTTCT 360

|||||
301 ACCAGATAGAGCTCGAGATTGGAGCTTTATTATTGCTGCAAGGTACACATTTTCCCT 360
|||||
361 CGGACGTTTCGGTGGAGGACCAAG 384
|||||
361 CGGACGTTTCGGTGGAGGACCAAG 384
|||||
RESULT 3
ADP45590
ID ADP45590 standard; cDNA; 717 BP.
XX
AC ADP45590;
XX
DT 09-SEP-2004 (first entry)
XX
DE Mouse binding molecule 11C7 light chain cDNA SEQ ID NO:44.
XX
KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
KW nerve repair; neuroprotective; gene therapy;
KW central nervous system injury; CNS injury; neurodegenerative disorder;
KW mouse; gene; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 1..717
CDS /*tag= a
FT /product= "binding molecule 11C7 light chain"
XX
WO2004052932-A2.
XX
24-JUN-2004.
XX
09-DEC-2003; 2003WO-EP013960.
XX
10-DEC-2002; 2002GB-00028832.
XX
(NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
PA (UYZU-) UNIV ZUERICH.
XX
Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;
PI Zurini M;
FI
XX
WPI; 2004-468818/44.
XX
New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.
XX
Example 5; SEQ ID NO 44; 121pp; English.
XX
The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA_623-640 with a dissociation constant of less than 100nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence encodes a mouse binding molecule 11C7 light chain, which is used in the exemplification of the present invention.
XX
SQ Sequence 717 BP; 194 A; 176 C; 175 G; 172 T; 0 U; 0 Other;
Query Match 93.6%; Score 370.6; DB 12; Length 717;
Best Local Similarity 96.4%; Pred. No. 6.3e-111; Indels 0; Gaps 0;
Matches 379; Conservative 0; Mismatches 14;

QY 4 ATGAGTCTGCCAGTTCTGTTCTTCTGTTAGTGTCTGATTTCGGGAACCAACGGTTAT 63
Db 1 ATGAGTCTGCCAGTTCTGTTCTTCTGTTAGTGTCTGATTTCGGGAACCAACGGTTAT 60
QY 64 GTTGTGATGACCCAGACTCCACTCACTTTTGTGGGTACCATTTGGACACCAAGCCTCCATC 123
Db 61 GTTCTGTTGACCCAGACTCTCTCTCATTTGTCGATAACCATTTGGACACCAAGCCTCCATC 120
QY 124 TCTTGCAGTCAAGTCAGAGCCTCTTAGATAGTAGTGAAGAAAGACATATTTGAATTGGTTG 183
Db 121 TCTTGCAGTCAAGTCAGAGCCTCTTGCATAGTAGTGAAGAAAGACATATTTGAATTGGTTG 180
QY 184 TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTCTAAATCGACTCT 243
Db 181 TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTCTAAATCGACTCT 240
QY 244 GGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGACAGAGATTTTACACTGAAAATCAGC 303
Db 241 GGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGACAGGATTTTACACTGAAAATCAGC 300
QY 304 AGAATAGAGGCTGAGGATTTGGGACTTTTATTATTGCTGGCAAGGTACACATTTTCTCGG 363
Db 301 AGAGTGGAGGCTGAGGATTTGGGACTTTTATTATTGCTGGCAAGGTACACATTTTCTCAG 360
QY 364 ACCTTCGGTGGAGGCCAGCCTGGAATCAAA 396
Db 361 ACCTTCGGTGGAGGCCAGCCTGGAATCAAA 393
RESULT 4
ABN84610
ID ABN84610 standard; cDNA; 420 BP.
XX
AC ABN84610;
XX
DT 29-OCT-2002 (first entry)
XX
DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VL coding region.
XX
KW Streptococcus mutans; monoclonal antibody; MAB; mouse; chimeric antibody;
KW antibody; anticaries; transgenic plant; transgenic animal; caries;
KW immunotherapy; therapy; gene; ss.
XX
OS Mus musculus.
FH Key Location/Qualifiers
FT 13..417
CDS /*tag= a
FT /partial
FT /product= "SWLA3 light chain variable region"
FT /note= "the CDS does not include a stop codon"
XX
US2002068066-A1.
XX
06-JUN-2002.
XX
15-JUN-2001; 2001US-00881823.
XX
20-AUG-1999; 99US-00378577.
XX
(SHIW/) SHI W.
PA (MORR/) MORRISON S L.
PA (TRIN/) TRINH K.
PA (WIMS/) WIMS L.
PA (CHEN/) CHEN L.
PA (ANDE/) ANDERSON M H.
XX
Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;
XX
WPI; 2002-565838/60.
DR P-PSDB; ABB79729.
XX
PT Treatment and prevention of dental caries in mammals, in particular

PT humans by orally administering genetically engineered or purified
XX antibodies that bind to surface antigens of carcinogenic organisms.

PS Claim 7; Fig 3A; 30pp; English.

XX The present sequence is the coding sequence of the light chain variable
CC region (VL) of the murine monoclonal antibody SWLA3 (IgG), which binds
CC specifically to the surface antigens of carlogenic type c Streptococcus
CC mutans (ATCC 25175). The coding sequence was obtained from SWLA3 (ATCC HB
CC 12558) hybridoma cells by PCR amplification (see also ABN84626 and
CC ABN84627). The SWLA3 VL and VH (see ABN84611) coding sequences were used
CC in the preparation of chimeric monoclonal antibody TERC comprising SWLA3
CC variable regions and human antibody constant regions. Such chimeric
CC monoclonal antibodies can be used to prevent or treat dental caries in
CC humans. The antibodies engage the effector apparatus of the human immune
CC system when they bind carcinogenic organisms, resulting in their
CC destruction. The antibodies may be produced in edible plants, in
CC transgenic animals, or in chicken eggs for oral ingestion
XX

SQ Sequence 420 BP; 99 A; 98 C; 112 G; 111 T; 0 U; 0 Other;

Query Match 93.1%; Score 368.8; DB 6; Length 420;
Best Local Similarity 95.7%; Pred. No. 1.9e-110;
Matches 379; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 ATGATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGGATTCCGGAAACCAACGGT 60

DB 13 ATGATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGGATTCCGGAAACCAACGGT 72

QY 61 TATGTTGATGACCCAGACTCCACTCACTTTGTGCGTTACCATGGACAACAGCTCC 120

DB 73 GATGTTGATGACCCAGACTCCACTCACTTTGTGCGTTACCATGGACAACAGCTCC 132

QY 121 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGATAGTATGGAAAGACATATTGATGG 180

DB 133 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGATAGTATGGAAAGACATATTGATGG 192

QY 181 TTGTTACAGAGCCAGCCAGTCTCCAAAGCGCTAATCTATCTGTTGCTAAACTGGAC 240

DB 193 TTGTTACAGAGCCAGCCAGTCTCCAAAGCGCTAATCTATCTGTTGCTAAACTGGAC 252

QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 300

DB 253 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 312

QY 301 ACCAGATAGAGGCTGAGATTTGGACCTTATTATTGCTGCGAAGGTACACATTTTCT 360

DB 313 ACCAGATAGAGGCTGAGATTTGGACCTTATTATTGCTGCGAAGGTACACATTTTCT 372

QY 361 CGGACGTTCCGTTGGAGCCACCAAGCTGGAAATCAAA 396

DB 373 CTCACGTTCCGTTGGAGCCACCAAGCTGGAGCTGAAA 408

RESULT 5

ADM72032

ID ADM72032 standard; DNA; 717 BP.

XX AC ADM72032;

XX DT 03-JUN-2004 (first entry)

XX DE Chimeric mouse-human antibody M3C11 light chain encoding DNA.

XX KW GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;

XX OS cytosolic; gene; ds; M3C11.

XX OS Mus sp.

XX OS Homo sapiens.

XX OS Chimeric.

XX FH Key

XX CDS Location/Qualifiers

1. .717

FT /*tag= a
XX /product= "M3C11 light chain"
XX PN WO2004022739-A1.

XX PD 18-MAR-2004.

XX PF 04-SEP-2003; 2003WO-JP011318.

XX PR 04-SEP-2002; 2002WO-JP008999.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;

XX WPI; 2004-269573/25.

XX DR P-PSDB; ADM72033.

XX PT Antibody against the N terminus of glypican 3 (GPC3) causes cell

XX disruption and is useful as an anticancer agent.

XX PS Example 4; SEQ ID NO 17; 122pp; Japanese.

XX CC The invention relates to an antibody against the N terminus of glypican 3

XX CC (GPC3). The antibody can be used for causing cell disruption and can be

XX CC used as an anti-cancer agent. The present sequence represents a chimeric

XX CC mouse-human antibody M3C11 light chain encoding DNA.

XX SQ Sequence 717 BP; 184 A; 180 C; 186 G; 167 T; 0 U; 0 Other;

Query Match 92.4%; Score 365.8; DB 12; Length 717;

Best Local Similarity 95.7%; Pred. No. 2.4e-109;

Matches 376; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 4 ATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGGATTCCGGAAACCAACGGTTAT 63

DB 1 ATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGGATTCCGGAAACCAACGGTTAT 60

QY 64 GTTGTGATGACCCAGACTCCACTCACTTTGTCGTTTACCATTGGACAACAGCTCCATC 123

DB 61 GTTGTGATGACCCAGACTCCACTCACTTTGTCGTTTACCATTGGACAACAGCTCCATC 120

QY 124 TCTTGAAGTCAAGTCAGAGCTCTTTAGATAGTATGGAAAGACATATTTGAATTGGTTG 183

DB 121 TCTTGAAGTCAAGTCAGAGCTCTTTAGATAGTATGGAAAGACATATTTGAATTGGTTG 180

QY 184 TTACAGAGCCAGCCAGTCTCCAAAGCGCTAATCTATCTGTTGCTAAACTGGACTCT 243

DB 181 TTACAGAGCCAGCCAGTCTCCAAAGCGCTAATCTATCTGTTGCTAAACTGGACTCT 240

QY 244 GGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATCAGC 303

DB 241 GGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATCAGT 300

QY 304 AGAATAGAGGCTGAGGATTTGGACTTTTATTATTGCTGCGAAGGTACACATTTTCTCGG 363

DB 301 AGAGTGGAGGCTGAGGATTTGGAAATTTATTATTGCTGCGAAGGTACACATTTTCTCGG 360

QY 364 AGTTCGGTGGAGGCCACCAAGCTGGAAATCAAA 396

DB 361 AGTTCGGTGGAGGCCACCAAGCTGGAGCTGAAA 393

RESULT 6

ABZ24632

ID ABZ24632 standard; cDNA; 717 BP.

XX AC ABZ24632;

XX DT 27-OCT-2003 (revised)

XX DT 31-MAR-2003 (first entry)

XX DE Humanised 3D6 antibody light chain cDNA.

XX Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
 KW human; humanised antibody; antibody; Alzheimer's disease;
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic;
 KW gene; 88.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key
 FT CDS
 FT Location/Qualifiers
 FT 1..717
 FT /*tag= a
 FT /product= "Humanised 3D6 antibody light chain"
 FT /partial
 FT /note= "the CDS does not include a stop codon"
 FT 1..60
 FT /*tag= b
 FT sig_peptide
 FT 61..717
 FT mat_peptide
 FT /*tag= c
 FT
 XX WO200288306-A2.
 XX
 XX 07-NOV-2002.
 PD
 XX 26-APR-2002; 2002WO-US011853.
 XX
 XX 30-APR-2001; 2001US-0287539P.
 XX
 XX (ELIL) LILLY & CO ELI.
 PA
 XX Tsurushita N, Vasquez M;
 PI
 XX WPI: 2003-183835/18.
 DR P-PSDB; ABP58274.
 DR
 XX New humanized forms of mouse 3D6 antibodies, useful for treating Down's
 PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
 PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta
 PT plaque in the brain.
 PT
 XX Claim 15; Page 12-13; 54pp; English.
 PS
 XX The present sequence is that of cDNA encoding a preferred light chain of
 CC a humanised antibody of the present invention. In the variable region of
 CC this sequence, the complementarity determining regions (CDRs) originate
 CC from murine monoclonal antibody 3D6 and the framework region from human
 CC germline V κ segment DPK19 and J segment Jk4. Novel humanised antibodies
 CC of the invention have CDRs from 3D6 and human framework sequences. These
 CC humanised antibodies have binding affinities (affinity and epitope
 CC location) approximately the same as those of the mouse 3D6 antibody. The
 CC invention includes antibodies, single chain antibodies, and their
 CC fragments, as well as nucleotide sequences, vectors, transformed host
 CC cells, and methods of using the humanised antibody to treat, prevent,
 CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
 CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
 CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
 CC reduce Abeta plaque in the brain. (Updated on 27-OCT-2003 to standardise
 CC OS field)
 XX
 SQ Sequence 717 BP; 182 A; 185 C; 185 G; 165 T; 0 U; 0 Other;
 Query Match 91.9%; Score 364; DB 8; Length 717;
 Best Local Similarity 94.9%; Pred. No. 9.3e-109;
 Matches 376; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ATGATGAGTCTCTGCCAGTTCCTGTTTCTGTAGTGTCTGTGATTCGGGAACCAACGGT 60
 DB 1 ATGATGAGTCTCTGCCAGTTCCTGTTTCTGTAGTGTCTGTGATTCGGGAACCAACGGT 60
 QY 61 TATGTTGTGATGACCCAGACTCCACTCCTTGTGCGTTACCATTTGGACACACAGCTCC 120
 DB 61 GATGTTGTGATGACCCAGTCTCCACTCTCTCTGCTTGTACCTTGGGACACAGCTCC 120

QY 121 ATCTCTTGCAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGGAAGACATATTTGAATGG 180
 DB 121 ATCTCTTGCAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGGAAGACATATTTGAATGG 180
 QY 181 TTGTTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAAATCTATCTGTGTCTTAAACTGGAC 240
 DB 181 TTGCAACAGGCCCCAGGCCAGTCTCCAAAGCGCCTAAATCTATCTGTGTCTTAAACTGGAC 240
 QY 241 TCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC 300
 DB 241 TCTGGAGTCCCTGACAGGTTTCTCTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC 300
 QY 301 AGCAGATAGAGGCTGAGGATTTGGGACTTTATTTATTGCTGGCAAGGTACACATTTTCC 360
 DB 301 AGCAGAGTTCGAGGCTGAGGATTTGGGAGTTTATTTATTGCTGGCAAGGTACACATTTTCC 360
 QY 361 CGGACGTTTCGTTGGAGGCCACCAAGCTGGAATCAAA 396
 DB 361 CGGACGTTTCGTTGGAGGCCACCAAGTGGAAATCAAA 396
 RESULT 7
 ABZ24634
 ID ABZ24634 standard; DNA; 1953 BP.
 XX
 AC ABZ24634;
 XX
 DT 27-OCT-2003 (revised)
 DT 31-MAR-2003 (first entry)
 XX
 DE Humanised 3D6 antibody light chain gene.
 XX
 KW Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
 KW human; humanised antibody; antibody; Alzheimer's disease;
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic;
 KW gene; ds.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key
 FT CDS
 FT Location/Qualifiers
 FT 12..1088
 FT /*tag= a
 FT /product= "Humanised antibody light chain"
 FT /note= "includes an intron"
 FT 12..408
 FT /*tag= b
 FT intron 409..765
 FT /*tag= c
 FT exon 766..1088
 FT /*tag= d
 FT polyA_signal 1261..1266
 FT /*tag= e
 XX WO200288306-A2.
 XX
 XX 07-NOV-2002.
 XX
 XX 26-APR-2002; 2002WO-US011853.
 XX
 XX 30-APR-2001; 2001US-0287539P.
 XX
 XX (ELIL) LILLY & CO ELI.
 XX
 XX Tsurushita N, Vasquez M;
 XX WPI: 2003-183835/18.
 DR P-PSDB; ABP58274.
 DR
 XX New humanized forms of mouse 3D6 antibodies, useful for treating Down's
 PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
 PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral

PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta
PT plaque in the brain.
PS Claim 15; Page 15; 54pp; English.
XX
CC The present sequence is that of the gene, including an intron, encoding a
CC humanised 3D6 light chain of the present invention. In the variable
CC region of this sequence, the complementarity determining regions (CDRs)
CC originate from murine monoclonal antibody 3D6 and the framework region
CC from human germline Vk segment DPK19 and J segment Jk4. Novel humanised
CC antibodies of the invention have CDRs from 3D6 and human framework
CC sequences. These humanised antibodies have binding affinities (affinity
CC and epitope location) approximately the same as those of the mouse 3D6
CC antibody. The invention includes antibodies, single chain antibodies, and
CC their fragments, as well as nucleotide sequences, vectors, transformed
CC host cells, and methods of using the humanised antibody to treat,
CC prevent, alleviate, reverse or otherwise ameliorate symptoms and/or
CC pathology associated with Down's syndrome, (pre-)clinical Alzheimer's
CC disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit
CC formation or reduce Abeta plaque in the brain. (Updated on 27-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 1953 BP; 548 A; 490 C; 384 G; 531 T; 0 U; 0 Other;

Query Match 91.9%; Score 364; DB 8; Length 1953;
Best Local Similarity 94.9%; Pred. No. 1.4e-108;
Matches 376; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ATGATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGATTCGGGAACCAACGGT 60
DB 12 ATGATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGATTCGGGAACCAACGGT 71
QY 61 TATGTTGTGATGACCCAGATCCACACTCTTTGTGGTTTACCATTCGCAACACAGCTCC 120
DB 72 GATGTTGTGATGACCCAGATCTCCTCTGCTGTTACCTCGGCAACACAGCTCC 131
QY 121 ATCTCTTGCAGAGTCAAGTCAGAGCTCTTATGATAGTATGATGGAAGACATATTGGAATTGG 180
DB 132 ATCTCTTGCAGAGTCAAGTCAGAGCTCTTATGATAGTATGGAAGACATATTGGAATTGG 191
QY 181 TTGTTACAGAGCCAGGCGAGTCTCAAGCGCTTAATCTATCTGTTGCTTAACCTGGAC 240
DB 192 TTGCAACAGCGCGCCAGGCGAGTCTCAAGCGCTTAATCTATCTGTTGCTTAACCTGGAC 251
QY 241 TCTGGAGTCCCTGACAGGTTCTACTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 300
DB 252 TCTGGAGTCCCTGACAGGTTCTCTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 311
QY 301 AGCAGAAATAGAGCTGAGGATTTGGGACTTTTATTTATTTGCTGGCAAGGTACACATTTTCT 360
DB 312 AGCAGAGTCCGAGGCTGAGGATTTGGGAGTTTATTTATTTGCTGGCAAGGTACACATTTTCT 371
QY 361 CGGACGTTTCGGTGGAGGCGACCAAGCTGGAAATCAAA 396
DB 372 CGGACGTTTCGGTGGAGGCGACCAAGCTGGAAATCAAA 407

RESULT 8
AAZ33016
ID AAZ33016 standard; DNA; 393 BP.
XX
AC AAZ33016;
XX
DT 26-JAN-2000 (first entry)
XX
DE Anti-tissue factor mouse monoclonal antibody ATR-7 L chain V region DNA.
XX
KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW disseminated intravascular coagulation; immunogenicity; chimeric; ss.
XX
OS Synthetic.
OS Mus sp.

XX WO9511743-A1.
XX 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-JP001768.
XX
PR 03-APR-1998; 98JP-00091850.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
XX Sato K, Adachi H, Yabuta N;
PI WPI; 1999-620204/53.
XX
DR P-PSDB; AAY52765.
XX
PT Humanised antibody recognizing human tissue factor, used for treatment of
PT disseminated intravascular coagulation.
XX
PS Example 1; Page 196-197; 291pp; Japanese.
XX
CC The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (hrf) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
CC containing the variable region of the L chain of a mouse monoclonal Ab
CC recognising human tissue factor (hrf) and the constant region of the L
CC chain of a human Ab, the variable region being one of six specified
CC sequences (which are the L chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
CC and prevention of thrombotic disease, especially of disseminated
CC intravascular coagulation (DIC). The humanised antibody has the high hrf
CC binding activity of the mouse monoclonal antibody but greatly reduced
CC immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAY52767 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 393 BP; 98 A; 85 C; 104 G; 106 T; 0 U; 0 Other;

Query Match 91.2%; Score 361; DB 2; Length 393;
Best Local Similarity 94.9%; Pred. No. 6.9e-108;
Matches 373; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 4 ATGAGTCTGCCAGTTCCTGTTCTGTTAGTGTCTCTGATTCGGGAACCAACCGTTAT 63
DB 1 ATGAGTCTGCCAGTTCCTGTTCTGTTAGTGTCTCTGATTCGGGAATCAACGGTAT 60
QY 64 GTTGTGATGACCCAGATCCACTCTTTGTCGGTTACCAATTGGACAACAGCCTCCATC 123
DB 61 GTTGTGCTGACCCAGATCCACTCTTTGTCGGTTACCAATTGGACAACAGCCTCCGTC 120
QY 124 TCTTGCAGTCAAGTCAGAGCTCTTAGATAGTATGGAAGACATATTTGATTTGGTTG 183
DB 121 TCTTGCAGTCAAGTCAGAGCTCTTAGATAGTATGGAAGACATATTTGATTTGGTTG 180
QY 184 TTACAGAGCCAGGCGAGTCTCAAGCGCTTAATCTATCTGTTGCTCTAACTGGACTCT 243
DB 181 TTACAGAGCCAGGCGAGTCTCAAGCGCTTAATCTATCTTGTGTCTTAACTGGACTCT 240
QY 244 GGAGTCCCTTGACAGGTTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 303
DB 241 GGAGTCCCTTGACAGGTTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 300
QY 304 AGAATAGAGCTGAGGATTTGGGACTTTTATTTATTTGCTGGCAAGGTACACATTTTCTCGG 363
DB 301 AGAGTGGAGGCTGAGGATTTGGGAGTTTATTTATTTGTTGCAAGATACACATTTTCCGGAC 360
QY 364 AGCTTCGGTGGAGGCGACCAAGCTGGAAATCAAA 396
DB 361 AGCTTCGGAGGGGGGACCAAGCTGGAAATCAAA 393

RESULT 9
AAZ33017
ID AAZ33017 standard; DNA; 393 BP.
XX
AC AAZ33017;
XX
DT 26-JAN-2000 (first entry)
XX
DE Anti-tissue factor mouse monoclonal antibody ATR-8 L chain V region DNA.
XX
KW Human tissue factor; TE; humanised; antibody; mouse monoclonal antibody;
KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW disseminated intravascular coagulation; immunogenicity; chimeric; ss.
OS Synthetic.
OS Mus sp.
XX
XX WO9951743-A1.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-JP001768.
XX
PR 03-APR-1998; 98JP-00091850.
XX
PA (CHUS) CHUGAI SBIYAKU KK.
XX
PI Sato K, Adachi H, Yabuta N;
XX
XX WPI; 1999-620204/53.
DR P-PSDB; AAY52766.
XX
XX Humanised antibody recognizing human tissue factor, used for treatment of
PT disseminated intravascular coagulation.
XX
XX Example 1; Page 197-198; 291pp; Japanese.
XX
XX The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (hTF) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
CC containing the variable region of the L chain of a mouse monoclonal Ab
CC recognising human tissue factor (hTF) and the constant region of the L
CC chain of a human Ab, the variable region being one of six specified
CC sequences (which are the L chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
CC and prevention of thrombotic disease, especially of disseminated
CC intravascular coagulation (DIC). The humanised antibody has the high hTF
CC binding activity of the mouse monoclonal antibody but greatly reduced
CC immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAY52767 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 393 BP; 99 A; 85 C; 103 G; 106 T; 0 U; 0 Other;

Query Match
Best Local Similarity 91.2%; Score 361; DB 2; Length 393;
Matches 373; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
XX
OY 4 ATGAGTCTGCCAGTCTCTGTTCTCTGTTAGTCTCTGATTCGGGAAACCAACGGTTAT 63
DB 1 ATGAGTCTGCCAGTCTCTGTTCTCTGTTAGTCTCTGATTCGGGATATCAACGGTAT 60
OY 64 GTTGTGATGACCCAGTCTCACTCTTGTGCGTTACATTTGGACACACCGCTCCATC 123
DB 61 GTTGTGATGACCCAGTCTCACTCTTGTGCGTTACATTTGGACACACCGCTCCGTC 120
OY 124 TCTTCAAGTCAAGTCAGAGCTCTTAGATAGTGATGAAAGACATATTTGAATGGTTG 183
DB 121 TCTTCAAGTCAAGTCAGAGCTCTTAGATAGTGATGAAAGACATATTTGAATGGTTG 180
OY 184 TTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAAATCTATCTGTTCTATAAAGTGGACTCT 243

DB 181 TTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAAATCTATCTGTTCTATAAAGTGGACTCT 240
OY 244 GGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 303
DB 241 GGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGACAGATTTTCACTGAAATCAGC 300
OY 304 AGAATAGAGGCTGAGGATTTGGGACTTTATTATTATTCTGGCAAGGTACACATTTTCTCGG 363
DB 301 AGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTATTGTTGGCAAGATACACATTTTCCGGAC 360
OY 364 ACCTTCGGTGGAGGACCAAGCTGGAATCAAA 396
DB 361 ACCTTCGGAGGGGGACCAAGCTGGAATCAAAA 393

RESULT 10
AAQ12063
ID AAQ12063 standard; DNA; 426 BP.
XX
AC AAQ12063;
XX
DT 25-MAR-2003 (revised)
DT 15-AUG-1991 (first entry)
XX
XX Sequence encoding light (kappa) chain variable region of murine 4D12
DE immunoglobulin.
XX
KW Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 31..426
FT /tag= a
FT /product= "mouse MAb 4D12 L(kappa)-chain variable region"
XX
PN WO9107493-A.
XX
PD 30-MAY-1991.
XX
PF 13-NOV-1989; 89US-00433730.
PR 13-NOV-1989; 89US-00433730.
XX
PA (XOMA) XOMA CORP.
PA (GREC) GREEN CROSS CORP.
XX
XX Better MD, Horwitz AH, Ghoshdaati P, Robinson R;
XX WPI; 1991-178105/24.
XX P-PSDB; AAR12361.
XX
XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT -1 antigen from sample.
XX
XX Disclosure; Fig 18; 107pp; English.
XX
XX This sequence encodes the light (kappa) chain variable (V) region of a
CC mouse monoclonal antibody (MAb), 4D12, specific for an HIV-1 viral
CC antigen. It is used in the construction of a chimeric MAB comprising
CC heavy and light chains having murine V regions and human C regions. The
CC chimeric MABs are more effective than murine MAB 4D12 since they have an
CC increased compatibility in humans. The heavy and light chain V-regions
CC are joined by manipulating their respective joining (J) regions, to
CC generate restriction enzyme recognition sites. The chimeric MABs can be
CC used as immuno- conjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
CC 62. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
XX to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
SQ Sequence 426 BP; 100 A; 99 C; 105 G; 122 T; 0 U; 0 Other;

XX 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250089P.
XX (JUNG/) JUNGHANS R P.
XX Junghans RP;
PI WPI; 2003-208946/20.
DR P-PSDB; ABG74244.

XX 25-MAR-2003 (revised)
DT 28-DEC-1992 (first entry)
XX Sequence of the chimeric kappa chain cDNA (lgkv) contained in pTB1427.
XX Chimeric monoclonal antibody; anti-fibrin antibody; primer;
KW antithrombotic agent; myocardial infarction therapy; ss.
XX Synthetic.

XX Claim 2; Fig 4E; 35pp; English.

XX The invention relates to a chimaeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC binding gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimaeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the anticancer therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence
CC encodes the mouse antibody 3D8 light chain variable region
XX

XX Sequence 729 BP; 203 A; 177 C; 172 G; 177 T; 0 U; 0 Other;

XX Query Match 90.9%; Score 359.8; DB 8; Length 729;
DR Best Local Similarity 94.4%; Pred. No. 2.2e-107;
DR Matches 373; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Qy 2 TGATGAGTCTGCCAGTTCCTGTTCTGTTAGTGTCTGATTCGGGAACCAACGGTT 61
Db 13 TGATGAGTCTGCCAGTTCCTGTTCTGTTAGTGTCTGATTCGGGAACCAACGGTG 72
Qy 62 ATGTTGTGATGACCCAGACTCCACTCACTTTGTGGTTACCATGGACAACAGCTTCA 121
Db 73 ATGTTGTGATGACCCAGACTCCACTCACTTTGTGGTTACCATGGACAACAGCTTCA 132
Qy 122 TCTCTTGCAGTCAAGTCAGAGCCTTTAGATAGTATGATGGAAGACATATTTGAATTGGT 181
Db 133 TCTCTTGCAGTCAAGTCAGAGCCTTTATATAGTATGGAAGAACCTATTTGAATTGGT 192
Qy 182 TGTTACAGAGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGGTGTCTAACTGGACT 241
Db 193 TATTACAGAGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGGTGTCTAACTGGACT 252
Qy 242 CTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACCTGAAATCA 301
Db 253 CTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACCTGAAATCA 312
Qy 302 GCAGATAGAGCTGAGGATTTGGGACTTTATATTTGCTGGCAGGTCACATTTTCTCTC 361
Db 313 GCAGATAGAGCTGAGGATTTGGGAGTTTATTTACTGCGTGCAGGTACACATTTTCTCTC 372
Qy 362 GCAGTCTCGTGGAGCCAGCTGGAATCAAA 396
Db 373 ACAGCTTCGAGGGGGGACCAAGCTGGAAATAAAA 407

XX Query Match 90.9%; Score 359.8; DB 8; Length 729;
DR Best Local Similarity 94.4%; Pred. No. 2.2e-107;
DR Matches 373; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2 TGATGAGTCTGCCAGTTCCTGTTCTGTTAGTGTCTGATTCGGGAACCAACGGTT 61
Db 13 TGATGAGTCTGCCAGTTCCTGTTCTGTTAGTGTCTGATTCGGGAACCAACGGTG 72
Qy 62 ATGTTGTGATGACCCAGACTCCACTCACTTTGTGGTTACCATGGACAACAGCTTCA 121
Db 73 ATGTTGTGATGACCCAGACTCCACTCACTTTGTGGTTACCATGGACAACAGCTTCA 132
Qy 122 TCTCTTGCAGTCAAGTCAGAGCCTTTAGATAGTATGATGGAAGACATATTTGAATTGGT 181
Db 133 TCTCTTGCAGTCAAGTCAGAGCCTTTATATAGTATGGAAGAACCTATTTGAATTGGT 192
Qy 182 TGTTACAGAGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGGTGTCTAACTGGACT 241
Db 193 TATTACAGAGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGGTGTCTAACTGGACT 252
Qy 242 CTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACCTGAAATCA 301
Db 253 CTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACCTGAAATCA 312
Qy 302 GCAGATAGAGCTGAGGATTTGGGACTTTATATTTGCTGGCAGGTCACATTTTCTCTC 361
Db 313 GCAGATAGAGCTGAGGATTTGGGAGTTTATTTACTGCGTGCAGGTACACATTTTCTCTC 372
Qy 362 GCAGTCTCGTGGAGCCAGCTGGAATCAAA 396
Db 373 ACAGCTTCGAGGGGGGACCAAGCTGGAAATAAAA 407

RESULT 13

AAQ25691 standard; cDNA; 737 BP.

XX AAQ25691;
AC AAQ25691;

XX Key Location/Qualifiers
DT sig_peptide 12..71
FT /*tag= a
FT /label= leader
FT CDS 72..410
FT /*tag= b
FT /product= "V-kappa"
FT CDS 134..731
FT /*tag= c
FT /product= "C-kappa"
PN EP491351-A2.
XX 24-JUN-1992.
XX 17-DEC-1991; 91EP-00121591.
XX 18-DEC-1990; 90JP-00413829.
XX 11-NOV-1991; 91JP-00294464.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Iwasa S, Tada H, Watanabe T;
XX WPI; 1992-209528/26.
XX P-PSDB; AAR24811.

XX Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
DT and heavy chain variable and constant for treating thrombotic conditions
XX e.g. myocardial infarction.
XX Example; Fig 9; 87pp; English.
XX Poly(A) + RNA was prep'd. from the anti-fibrin chimeric Ab-producing
CC transformant FIB1-H01/X63 and used as a template to clone human C-kappa
CC cDNA, using the oligo-dT (Pharmacia) primer as a primer for first strand
CC cDNA, synthesis and the 3'E-kappa and 5'C-kappa primers for the PCR. An
CC amplified DNA fragment of about 0.33kb was isolated and used to create a
CC C-kappa cDNA contg. vector, pTB1394. Using the same technique, with the
CC 3'E-kappa primer as a primer for first strand synthesis and the 5'L-kappa
CC and 3'C-kappa primers for the PCR, an anti-fibrin V-kappa (V-kappa-v)
CC cDNA was amplified. Furthermore, using the 3'E-kappa primer for first
CC stand synthesis and the 5'mv-kappa and 3'mv-kappa primers for the PCR, an
CC anti-fibrin V-kappa cDNA (V-kappa-FIB) was amplified. In addition, a
CC leader sequence cDNA (L-kappa) was amplified using the 3'C-kappa as a
CC primer for first strand synthesis and the 5'S-kappa and 3'L-kappa
CC primers for the PCR. The amplified gene fragments (L-kappa: V-kappa-v; V-
CC kappa-FIB) were isolated and used to construct respectively plasmids
CC pTB1391, pTB1392, and pTB1393. L-kappa, V-kappa and C-kappa were joined
CC together to give a plasmid, pTB1427, contg. the whole length of the
CC chimeric kappa chain cDNA. (Updated on 25-MAR-2003 to correct PN field.)
XX

XX Sequence 737 BP; 186 A; 187 C; 189 G; 175 T; 0 U; 0 Other;

XX Query Match 87.1%; Score 344.8; DB 2; Length 737;
DR Best Local Similarity 91.9%; Pred. No. 1.9e-102;
DR Matches 364; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 1 ATGATGAGTCTGCCAGTTCCTGTTCTGTTAGTGTCTGATTCGGGAACCAACGGT 60
Db 12 ATGATGAGTCTGCCAGTTCCTGTTCTGTTAGTGTCTGATTCGGGAACCAACGGT 71

RESULT 15
ADQ89317
ID ADQ89317 standard; DNA; 426 BP.
XX
AC ADQ89317;
XX
DT 21-OCT-2004 (first entry)
XX
DE Mouse immunoglobulin DNA #1.
XX
KW Mouse; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;
KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
KW anti-HIV; virucide; antiarteriosclerotic; gene; ds.
XX
OS Mus musculus.
XX
PN US2004151721-A1.
XX
PD 05-AUG-2004.
XX
PP 10-DEC-2003; 2003US-00733563.
XX
PR 19-OCT-2001; 2001US-0350166P.
PR 26-JUN-2002; 2002US-0392364P.
PR 17-OCT-2002; 2002US-00272899.
XX
PA (OKEE/) O'KEEFE T.
PA (PONA/) PONA TH P.
XX
FI O'keefe T, Ponath P;
XX
XX WPI; 2004-580175/56.
DR P-PSDB; ADQ89324.
XX
XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
PT useful for diagnosing and/or treating inflammatory or autoimmune
PT diseases, and HIV infection.
XX
PS Disclosure; SEQ ID NO 95; 128pp; English.
XX
XX The invention relates to humanised immunoglobulin heavy and light chains
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
CC immunoglobulin or its antigen binding fragment comprising the chains. The
CC humanised immunoglobulin or its antigen binding fragment preferably
CC comprises two heavy chains and two light chains. The humanised
CC immunoglobulin and its heavy and light chains are useful for the
CC diagnosis, prevention and/or treatment of diseases or conditions
CC associated with aberrant expression or activity of the CCR2 polypeptide,
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
CC infection and atherosclerosis. This sequence represents DNA encoding a
CC mouse immunoglobulin protein of the invention.
XX
SQ Sequence 426 BP; 104 A; 97 C; 114 G; 111 T; 0 U; 0 Other;
Query Match 84.7%; Score 335.4; DB 13; Length 426;
Best Local Similarity 94.3%; Pred. No. 1.8e-99;
Matches 348; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 28 CTGTTAGTCTCGATCGGGAACCAACGGTTATGTTGTGATGACCCAGACTCCACTC 87
DB 19 CTGTTGGTGTCTCGATTCGGGAGACAAATCGCGGATGTTGTGATGACCCAGACTCCACTC 78
QY 88 ACTTTGTCGGTTACCATTTGGACAACAGGCTTCATCTCTTGCAGTCAAGTCAGAGCCTC 147
DB 79 ACTTTGTCGGTTACCATTTGGACAACAGGCTTCATCTCTTGCAGTCAAGTCAGAGCCTC 138
QY 148 TTAGATAGTGTGGAAGACATATTTGAATTGGTTGTTTACAGAGCCAGGCCAGTCTCCA 207
DB 139 TTAGATAGTGTGGAAGACATATTTTGAATTGGTTGTTTACAGAGCCAGGCCAGTCTCCA 198
QY 208 AAGCCCTAATCTATCTGGTGTCTAAACTGGACTCTGGAGTCCCTGCACAGGTTCACTGGC 267

Db 199 AAGCGCCTAATCTATCTGGTGTCTAAACTGGACTCTGGAGTCCCTGCAGAGTTCACTGGC 258
QY 268 AGTGGATCAGGGACAGATTTTACACTGAAATCAGCAGAAATAGAGGCTGAGGATTTGGGA 327
Db 259 AGTGGATCAGGGACAGATTTTACACTGAAATCAGCAGAGTGGAGGCTGAGGATTTGGGA 318
QY 328 CTTTATTATTGCTGGCAAGGTACACATTTTCTCGGAGCTTCGGTGGAGGCCACCAAGCTG 387
Db 319 GTTTATTATTGCTGGCAAGGTACACATTTTCTCGGAGCTTCGGAGGGGGGACCAAGCTG 378
QY 388 GAATATCAA 396
Db 379 GAAATAAAA 387
Search completed: September 26, 2005, 05:09:03
Job time : 397 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 26, 2005, 05:48:07 ; Search time 90 Seconds
(without alignments)
751.049 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692
Sequence: 1 MMSPAQFLFLVLVIRETNG.....CWQTHPRPTFGGKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	511	73.8	239	2 Q8TCD0	Q8tcd0 homo sapien
2	508	73.4	133	1 KV2F HUMAN	P06310 homo sapien
3	471	68.1	239	2 Q8NEK0	Q8nek0 homo sapien
4	471	68.1	239	2 Q6P491	Q6p491 homo sapien
5	444.5	64.2	114	2 Q9UL80	Q9ul80 homo sapien
6	441.5	63.8	240	2 Q6PIH6	Q6pih6 homo sapien
7	434	62.7	113	1 KV2G MOUSE	P01631 mus musculus
8	430	62.1	219	2 Q65ZC0	Q65zco mus musculus
9	425	61.4	248	2 Q65ZQ7	Q65zq7 mus sp. b3(
10	417	60.3	117	1 KV2E HUMAN	P06309 homo sapien
11	415	60.0	113	1 KV2D HUMAN	P01617 homo sapien
12	414.5	59.9	115	1 KV2A HUMAN	P01614 homo sapien
13	414	59.8	113	1 KV2B HUMAN	P01615 homo sapien
14	389.5	56.3	112	1 KV2C HUMAN	P01616 homo sapien
15	388	56.1	113	1 KV2F MOUSE	P01630 mus musculus
16	386	55.8	129	1 KV3L HUMAN	P18135 homo sapien
17	381	55.1	112	2 Q6LEM8	Q6lem8 mus musculus
18	380.5	55.0	134	1 KV4C HUMAN	P06314 homo sapien
19	380	54.9	113	1 KV2E MOUSE	P03976 mus musculus
20	377.5	54.6	236	2 Q6PIL8	Q6pil8 homo sapien
21	376	54.3	235	2 Q6GMV9	Q6gmv9 homo sapien
22	374	54.0	112	1 KV2D MOUSE	P01629 mus musculus
23	374	54.0	120	1 KV2B MOUSE	P01627 mus musculus
24	373.5	54.0	131	1 KV3I MOUSE	P01661 mus musculus
25	373	53.9	113	1 KV2C MOUSE	P01628 mus musculus
26	373	53.9	129	1 KV3M HUMAN	P18136 homo sapien
27	373	53.9	133	1 KV4B HUMAN	P06313 homo sapien
28	369	53.3	112	1 KV2A MOUSE	P01626 mus musculus
29	368.5	53.3	236	2 Q6P5S8	Q6p5s8 homo sapien
30	363.5	52.5	108	1 KV1 CANFA	P01618 canis faml
31	362.5	52.4	236	2 Q7TS98	Q7ts98 mus musculus

32	358.5	51.8	111	1 KV3L MOUSE	P01664 mus musculus
33	358.5	51.8	128	1 KV3K HUMAN	P06311 homo sapien
34	357	51.6	129	1 KV3H HUMAN	P04207 homo sapien
35	355.5	51.4	255	2 Q6KB05	Q6kb05 mus musculus
36	353.5	51.1	111	1 KV3M MOUSE	P01665 mus musculus
37	353.5	51.1	111	1 KV3O MOUSE	P01667 mus musculus
38	352.5	50.9	111	1 KV3N MOUSE	P01666 mus musculus
39	351	50.7	235	2 Q6PJF2	Q6pjf2 homo sapien
40	350.5	50.7	128	1 KV5E MOUSE	P01637 mus musculus
41	348.5	50.4	111	1 KV3Q MOUSE	P01669 mus musculus
42	348.5	50.4	111	1 KV3R MOUSE	P01670 mus musculus
43	348.5	50.4	111	2 Q811U6	Q811u6 mus musculus
44	347.5	50.2	238	2 Q66J57	Q66j57 mus musculus
45	347	50.1	110	1 KV3P MOUSE	P01668 mus musculus

ALIGNMENTS

RESULT 1

ID	Q8TCD0	PRELIMINARY;	PRT;	239 AA.
AC	Q8TCD0;			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uesdin T.B., Toshitoki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marz M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RA	Strausberg R.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBDJ databases.			
DR	EMBL; BC022362; AAH22362.1; --			
DR	PIR; S22658; S22658.			
DR	PIR; S34095; S34095.			
DR	PIR; S40324; S40324.			
DR	PIR; S40374; S40374.			
DR	PIR; S42267; S42267.			
DR	PIR; S42268; S42268.			
DR	HSSP; P01834; 1172.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig ci.			
DR	InterPro; IPR003006; Ig MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF07654; C1-set; 1.			

FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009BE CRC64;

Query Match 73.4%; Score 508; DB 1; Length 133;
Best Local Similarity 73.5%; Pred. No. 2.6e-41;
Matches 97; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNQVVMVTQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLW 60
DB 1 MRLPAQLJGLLMLWPGSSGDVVMVTQSPUSLPTVLGQPASISCRSSQSLVSDGTYLW 60
QY 61 LLQRQGSQPKLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRBAEDLGLYYCQGHFP 120
DB 61 FOQRFGQSPRLIYKVNRSNDSGVPDRFSGSGTDFTLKISRBAEDVGVYFCQGHFP 120
QY 121 RTFGGQTKLEIK 132
DB 121 WTFGGQTKLEIK 132

RESULT 3
Q8NEKO PRELIMINARY; PRT; 239 AA.

ID Q8NEKO
AC Q8NEKO;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC030814; AAH30814.1; --
DR PIR, S23638; S23638.
DR PIR, S34091; S34091.
DR PIR, S40342; S40342.
DR PIR, S40357; S40357.
DR HSSP, P01834; I172.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.


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DR PROSITE; PSS0835; IG_LIKE; 2.  
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;  
  
Query Match 68.1%; Score 471; DB 2; Length 239;  
Best Local Similarity 68.2%; Pred. No. 1.9e-37;  
Matches 90; Conservative 19; Mismatches 23; Indels 0; Gaps 0;  
  
QY 1 MMSPAQFLVLVLTRETNQVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMW 60  
DB 1 MRLPAQLGLMLVSGSGDIVMTQSPVPTGEPASISCKSSQSLDSDGKTYLNMW 60  
QY 61 LLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGDTFTLKISRIEADLGLYYCWQGTTHP 120  
DB 61 YLQKPGSQPLLILYLVSKLDSGVPDRFTGSGSGDTFTLKISRIEADLGLYYCWQGTTHP 120  
QY 121 RTFGGQTKLEIK 132  
DB 121 QTFGQGTKEIK 132  
  
RESULT 4  
QP491  
ID Q6P491 PRELIMINARY; PRT; 239 AA.  
AC Q6P491;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RA Strausberg R.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC063599; AAH63599.1; -;  
DR HSSP; P01837; 1KCU.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.
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DR SMART; SM00406; IGv; 1.  
DR PROSITE; PSS0835; IG_LIKE; 2.  
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;  
  
Query Match 68.1%; Score 471; DB 2; Length 239;  
Best Local Similarity 68.8%; Pred. No. 1.9e-37;  
Matches 88; Conservative 21; Mismatches 19; Indels 0; Gaps 0;  
  
QY 5 AQFLFLVLVLTRETNQVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMW 64  
DB 5 AQLGLGLMLVSGSGDIVMTQSPVPTGEPASISCKSSQSLDSDGKTYLNMW 64  
QY 65 PQGSPKRLIYLVSKLDSGVPDRFTGSGSGDTFTLKISRIEADLGLYYCWQGTTHPRTFG 124  
DB 65 PQGPPRLIYKISNRFSGVDPDRFSGSGAGTFTLKISRVEADVGVYVCMQVHPRTFG 124  
QY 125 GGTKEIK 132  
DB 125 QGTRVEIK 132  
  
RESULT 5  
Q9UL80  
ID Q9UL80 PRELIMINARY; PRT; 114 AA.  
AC Q9UL80;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035034; AAD56270.1; -;  
DR PIR; B49002; B49002.  
DR PIR; S23638; S23638.  
DR PIR; S34094; S34094.  
DR PIR; S34095; S34095.  
DR HSSP; P01625; 1LVE.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG_v.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PSS0835; IG_LIKE; 1.  
FT NON TER 1  
FT NON TER 114  
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;  
  
Query Match 64.2%; Score 444.5; DB 2; Length 114;  
Best Local Similarity 76.8%; Pred. No. 3.2e-35;  
Matches 86; Conservative 12; Mismatches 13; Indels 1; Gaps 1;  
  
QY 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMWLPQSPKRLIYLVSKLDS 81  
DB 2 VVMTQSPSLPVLTRQPAISCKSSQSPVSGDNTYLNWFOQRPQSPKRLIYKVSNRDS 61  
QY 82 GVPDRFTGSGSGDTFTLKISRIEADLGLYYCWQGTTHPRTFGGQTKLEIK 132  
DB 62 GVPDRFTGSGSGDTFTLKISRVEADVGVYVCMQGTTHPRTFGGQTKVEIK 113  
  
RESULT 6  
QGPIH6
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ID Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC O6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zerbino B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.J.
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034142; AAH34142.1; -.
DR HSSP; P01837; 1KBS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

Query Match 63.8%; Score 441.5; DB 2; Length 240;
Best Local Similarity 66.2%; Pred. No. 1.4e-34;
Matches 88; Conservative 17; Mismatches 27; Indels 1; Gaps 1;

QY 1 MMSPAQLFLVLWIRETNQYVMTQTPLTSVTIGQPASISCKSSQSLDSDGKTYLW 60
DB 1 MRLPAQLGLLMLWVGSGSDIVMAQSPLSVTPGEPASISCRSSQSLHNSGNYNFDW 60

QY 61 LLORPGOSPKRLIYLYSKLDSGVPDRFTGSGSGTDFTLKISRVEADLGLYCWQTHF- 119
DB 61 YLQKPGSQQLLIYWGSGNRASGVPDRFSGSGSGTDFTLKISRVEADVGYYQMALQTP 120

QY 120 PRTFGGQTKLEIK 132
DB 121 PYTFGGQTKLEIK 133

RESULT 7
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KV2G MOUSE
ID KV2G MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RL anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS; This chain was isolated from an Igg2a hybridoma
CC protein that binds digoxin.
DR PIR; A01914; KMS26.
DR HSSP; Q95M37; 1I91.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 62.7%; Score 434; DB 1; Length 113;
Best Local Similarity 75.7%; Pred. No. 3.3e-34;
Matches 84; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 22 VVMTOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLWLLQRPQSPKRLIYLYSKLDS 81
DB 2 VVMTOTPLSLPVSGLGQASISCRSSQSLVHSGNTYLNWYLOKAGOSPRLIYKVSRRFS 61

QY 82 GVPDRFTGSGSGTDFTLKISRVEADLGLYCWQTHFPRFTGGGQTKLEIK 132
DB 62 GVPDRFSGSGSGTDFTLKISRVEADLGIYFCSQTHVPTFGGQTKLEIK 112

RESULT 8
Q65ZCO PRELIMINARY; PRT; 219 AA.
ID Q65ZCO;
AC Q65ZCO;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
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RT allergen Chi t I.";  
RL Int. Arch. Allergy Immunol. 110:348-353(1996).  
DR EMBL; Z37499; CAA85724.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig_c1.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 2.  
DR Pfam; PF0654; C1-set; 1.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00407; Ig_c1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG_LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.  
FT NON_TER 1  
FT NON_TER 219  
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAP8445 CRC64;  
  
Query Match 62.1%; Score 430; DB 2; Length 219;  
Best Local Similarity 73.0%; Pred. No. 1.6e-33;  
Matches 81; Conservative 16; Mismatches 14; Indels 0; Gaps 0;  
  
QY 22 VVMTQPTLTSLVTIGQPASISCKSSQSLDSDGKTYLWLLQRPQSPKRLIYLVSKLDS 81  
DB 2 LVMTQPSLSVSLGDAQISCRSSQSLVHTNGNTYLHWYLOKPGSLPKLIYIVSNRFS 61  
  
QY 82 GVPDRFTSGSGTDFTLKISRVEAEDLGLYCQWQTHPPRTFGGQTKLEIK 132  
DB 62 GVPDRFSGSGTDFTLKISRVEAEDLGLYFCSQTHVPGTFGGQTKLEIK 112  
  
RESULT 9  
Q65207 PRELIMINARY; PRT; 248 AA.  
AC Q65207;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE B3(FV)-PE40 (Fragment).  
GN Name=B3(FV)-PE40;  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92020904; PubMed=1924323;  
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;  
RT "B3(FV)-PE38KDEL, a single-chain immunotoxin that causes complete  
regression of a human carcinoma in mice."  
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).  
DR EMBL; S57990; AAB19971.2; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG_LIKE; 2.  
FT NON_TER 248  
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43B570950 CRC64;  
  
Query Match 61.4%; Score 425; DB 2; Length 248;  
Best Local Similarity 72.1%; Pred. No. 5.8e-33;  
Matches 80; Conservative 15; Mismatches 16; Indels 0; Gaps 0;  
  
QY 22 VVMTQPTLTSLVTIGQPASISCKSSQSLDSDGKTYLWLLQRPQSPKRLIYLVSKLDS 81  
DB 137 VLMTQPSLSVSLGDAQISCRSSQIIIVHNGNTYLEWYLOKPGSPKLIYIVSNRFS 196  
  
QY 82 GVPDRFTSGSGTDFTLKISRVEAEDLGLYCQWQTHPPRTFGGQTKLEIK 132  
DB 62 GVPDRFSGSGTDFTLKISRVEAEDLGLYFCSQTHVPGTFGGQTKLEIK 112
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Db 197 GVPDRFSGSGTDFTLKISRVEAEDLGLYFCSQSHVPTFGSGTKLEIK 247  
RESULT 10  
KV2E_HUMAN STANDARD; PRT; 117 AA.  
AC P06309;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region GM607 precursor (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84191506; PubMed=6325927;  
RA Klobeck H.G., Solomon A., Zachau H.G.;  
RT "Contribution of human V kappa II germ-line genes to light-chain  
diversity."  
RL Nature 309:73-76(1984).  
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or send an email to license@isb-sib.ch).  
CC EMBL; Z00009; -; NOT ANNOTATED_CDS.  
DR PIR; A01889; K2HUGM.  
DR HSP; Q99M37; 1191.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT NON_TER 1  
FT SIGNAL <1 4  
FT CHAIN 5 117 Ig kappa chain V-II region GM607.  
FT DOMAIN 5 27 Framework-1.  
FT DOMAIN 28 43 Complementarity-determining-1.  
FT DOMAIN 44 58 Framework-2.  
FT DOMAIN 59 65 Complementarity-determining-2.  
FT DOMAIN 66 97 Framework-3.  
FT DOMAIN 98 106 Complementarity-determining-3.  
FT DOMAIN 107 116 Framework-4.  
FT DISULFID 27 97 By similarity.  
FT NON_TER 117  
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;  
  
Query Match 60.3%; Score 417; DB 1; Length 117;  
Best Local Similarity 69.6%; Pred. No. 1.5e-32;  
Matches 80; Conservative 17; Mismatches 18; Indels 0; Gaps 0;  
  
QY 18 TNGYVMTQPTLTSLVTIGQPASISCKSSQSLDSDGKTYLWLLQRPQSPKRLIYLV 77  
DB 2 SSGDIVMTQPSLSLPTVTPGEPASISCRSSQSLHSHNGYVLDWYLOKPGSQPLLILGS 61  
  
QY 78 KLDGSDPDRFSGSGTDFTLKISRVEAEDLGLYCQWQTHPPRTFGGQTKLEIK 132  
DB 62 NRASGSDPDRFSGSGTDFTLKISRVEAEDGVVYCMQGLQTPQTFGGQTKVEIK 116  
  
RESULT 11  
KV2D_HUMAN STANDARD; PRT; 113 AA.
```



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DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 59.8%; Score 414; DB 1; Length 113;
Best Local Similarity 69.4%; Pred. No. 2.8e-32;
Matches 77; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 22 VVMTQPTLTLSVTIGQPASISCKSSQSLSDSGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 IVVTQSPFLPVTLPGEPAISCRSSQNLLZSBGB-YLDWYLZKFGZSPZLLIYLSNRAS 60

Qy 82 GVPDRFTGSGGTDFTLKISRIBAEADLGLYYCWQGTTHPRFTFGGTTKLEIK 132
Db 62 GVPDRFSDSGGTDFTLKIRVQAEADVGVYVCMQATZSPYTFGGTQKLZIK 112

RESULT 14
KV2C HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -I- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
DR PIR; A01913; KVM57S.
DR HSP; Q99M37; I191.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 112 AA; 12055 MW; E5B2E2FA7ABE481 CRC64;

Query Match 56.3%; Score 389.5; DB 1; Length 112;
Best Local Similarity 67.6%; Pred. No. 9.3e-30;
Matches 75; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
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Best Local Similarity 63.1%; Pred. No. 6.6e-30;
Matches 70; Conservative 24; Mismatches 16; Indels 1; Gaps 1;

Qy 22 VVMTQPTLTLSVTIGQPASISCKSSQSLSDSGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 IVVTQSPFLPVTLPGEPAISCRSSQNLLZSBGB-YLDWYLZKFGZSPZLLIYLSNRAS 60

Qy 82 GVPDRFTGSGGTDFTLKISRIBAEADLGLYYCWQGTTHPRFTFGGTTKLEIK 132
Db 61 GVPDRFSGSGGTFTLKISRVAZABGVYVCMQALQTLTFTFGGTTNVEIK 111

RESULT 15
KV2F MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -I- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
DR PIR; A01913; KVM57S.
DR HSP; Q99M37; I191.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 56.1%; Score 388; DB 1; Length 113;
Best Local Similarity 67.6%; Pred. No. 9.3e-30;
Matches 75; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
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Job time : 91 secs

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